

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	50.8	3.3	305312	6	US-10-995-561-13236	Sequence 13235, App
C 2	45.2	2.9	158692	7	US-11-121-086-30	Sequence 30, App
C 3	45	2.9	201990	6	US-10-995-561-13303	Sequence 13303, App
C 4	44.6	2.9	190365	6	US-10-995-561-13314	Sequence 13314, App
C 5	43.8	2.8	173602	7	US-11-121-086-25	Sequence 25, App
C 6	43.6	2.8	110000	7	US-11-155-492-1	Sequence 1, App
C 7	43.6	2.8	139054	7	US-11-121-086-96	Sequence 96, App
C 8	42.4	2.8	98716	6	US-10-995-561-13331	Sequence 13331, App
C 9	42.4	2.8	513	6	US-10-793-626-1925	Sequence 1925, App
C 10	42.4	2.8	2901	6	US-10-793-626-3425	Sequence 3425, App
C 11	42.4	2.8	173602	7	US-11-121-086-25	Sequence 25, App
C 12	42	2.7	1659	6	US-10-750-185-64246	Sequence 64246, App
C 13	41.8	2.7	4063	6	US-10-750-185-65813	Sequence 65813, App
C 14	41.8	2.7	105550	6	US-10-995-561-13235	Sequence 13235, App
C 15	41.6	2.7	13553	6	US-10-750-185-38081	Sequence 38081, App
C 16	41.6	2.7	15142	7	US-11-121-086-37	Sequence 37, App
C 17	41.4	2.7	1496	6	US-10-750-185-3143	Sequence 3143, App
C 18	41.4	2.7	150437	7	US-11-112-908-43	Sequence 44, App
C 19	41.4	2.7	1750491	7	US-11-112-908-46	Sequence 46, App
C 20	41.4	2.7	172543	7	US-11-121-086-6	Sequence 6, App
C 21	41.4	2.7	182314	7	US-11-112-908-45	Sequence 45, App
C 22	41.4	2.7	611587	7	US-11-117-187-209	Sequence 209, App
C 23	41.2	2.7	155781	7	US-11-121-086-32	Sequence 32, App

C	24	41	2.7	1292	6	US-10-750-185-55224	A	Sequence 55224, A
C	25	40.8	2.7	1201	6	US-10-995-561-55865	A	Sequence 28655, A
C	26	40.4	2.6	1011	6	US-10-750-185-26541	A	Sequence 26541, A
C	27	40.4	2.6	103931	7	US-11-117-187-193	A	Sequence 193, A
C	28	40.2	2.6	146656	7	US-11-121-086-68	A	Sequence 68, Appl
C	29	39.8	2.6	3127	6	US-10-793-626-51768	A	Sequence 37676, Ap
C	30	39.8	2.6	3157	6	US-10-793-626-1668	A	Sequence 3668, Ap
C	31	39.6	2.6	340000	7	US-11-102-978-3	Appl	Sequence 3, Appl
C	32	39.6	2.6	1082314	7	US-11-117-187-211	App	Sequence 211, App
C	33	39.6	2.6	1490	6	US-10-750-185-46942	A	Sequence 46942, A
C	34	39.4	2.6	5592	7	US-11-192-927-5	Appl	Sequence 5, Appl
C	35	39.4	2.6	5592	7	US-11-193-715-5	Appl	Sequence 5, Appl
C	36	39.4	2.6	184868	7	US-11-121-086-88	Appl	Sequence 88, Appl
C	37	39.4	2.6	1082144	7	US-11-117-187-211	Appl	Sequence 211, Appl
C	38	39.2	2.6	2036	6	US-10-986-217A-8	Appl	Sequence 8, Appl
C	39	39.2	2.6	26772	6	US-10-995-561-13313	A	Sequence 13313, A
C	40	39.2	2.6	54946	6	US-10-995-561-13479	A	Sequence 13479, A
C	41	39.2	2.6	125552	7	US-11-121-086-1	Appl	Sequence 1, Appl
C	42	39	2.5	2162	6	US-10-750-185-00667	A	Sequence 0667, A
C	43	39	2.5	3201	7	US-11-145-703-804	App	Sequence 204, App
C	44	39	2.5	148200	7	US-11-121-086-90	Appl	Sequence 90, Appl
C	45	39	2.5	153142	7	US-11-121-086-27	Appl	Sequence 27, Appl

ALIGNMENTS

```

RESULT 1
US-10-995-561-13236/c
Sequence 13236, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13236
LENGTH: 305312
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(305312)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13236

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Query Match	3.3%	Score 50.8;	DB 6;	Length 305312;
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Matches 91; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

1369 ATCCTACTCCTGAATTGATTGATAATATTTTCATCATGTTTTATATTTTATAAATTTTA 1428

[illegible]

1429 CTAATTACATGACAATTTATGGACTAAGTTACTTATTATATGTTTATTATATTGGA 1488

[illegible]

1489 AATGTGTTTAACTTACATAAAATTGCAATTAGTTTAA 1526

[illegible]

3
3
1
1
3
3

S-11-121-086-30/c

Publication No. US20050266459A1
CENTRAL INTELLIGENCE AGENCY

APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138, 6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIORITY FILING DATE: 2004-05-04
PRIORITY FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 30
LENGTH: 158692
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-30

Query Match 2.9%; Score 45.2; DB 7; Length 158692;
Best Local Similarity 56.8%; Pred. No. 1.3;
Matches 83; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

1383 TTGATTCATATATTTTCATCATGTTTATATTTTATTAATTTTACTAAATTTACATGA 1442
154813 TGTATATTAATTAATTTGCTATTAATGTTTAACTGAATTAATAATGCAATTTATTCATCA 154754
1443 CAATTTATGAGCTAAGTACTTATTTATGTTTATTAATTTGAATGCTTTTAAGT 1502
154753 AAAATTCATTAACCAATTAATTTTAAATATTCCTTCCTTAAGCATTTGTATTAAGT 154694
1503 TACATTAATTTGCAATTAGTTTAAA 1528
154693 TCATTAATAAATAATTAATAATGAAA 154668

RESULT 3
US-10-995-561-13303/C
Sequence 13303, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13303
LENGTH: 201990
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(201990)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13303

Query Match 2.9%; Score 45; DB 6; Length 201990;
Best Local Similarity 56.4%; Pred. No. 1.7;
Matches 84; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

1389 TGATATATTTTCATCATGTTTATATTTTATTAATTTTACTAAATTTACATGACATTT 1448
78616 TAAATTAATTAATTTTATTAATTAATTAATTTTATTAATTAATTAATTAATTAATTTTA 78557
1449 ATGAGCTAAGTACTTATTTATGTTTATTAATTTGAATGCTTTTAAGTTACATA 1508
78556 TTTTAAATTAATTAATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTTTAA 78497
1509 AAATGCAATTAGTTTAAAAAAA 1537
78496 TATTTCTGCTCTCTGTTGAGGGGAAAAA 78468

RESULT 4
US-10-995-561-13314/C
Sequence 13314, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13314
LENGTH: 119036
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(119036)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13314

Query Match 2.9%; Score 44.6; DB 6; Length 119036;
Best Local Similarity 55.5%; Pred. No. 1.6;
Matches 86; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

1383 TTGATTCATATATTTTCATCATGTTTATATTTTATTAATTTTACTAAATTTACATGA 1442
31696 TTATATTAATTAATTAATTTTATTAATTAATTTTATTAATTAATTAATTAATTAATTTCA 31637
1443 CAATTTATGAGCTAAGTACTTATTTATGTTTATTAATTTGAATGCTTTTAAGT 1502
31636 TATTTAAATTAATTAATTAATTTTATTAATTAATTTTATTAATTAATTAATTAATTTCT 31577
1503 TACATTAATTTGCAATTAGTTTAAAAAAA 1537
31576 TATTTATTAATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTTCA 31542

RESULT 5
US-11-121-086-25/C
Sequence 25, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138, 6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIORITY FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 25
LENGTH: 173602
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-25

Query Match 2.8%; Score 43.8; DB 7; Length 173602;
Best Local Similarity 55.6%; Pred. No. 3.3;
Matches 84; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

1387 ATGATATATTTTCATCATGTTTATATTTTATTAATTTTACTAAATTTACATGACAT 1446
136252 ATTATATTAATTAATTAATTTTATTAATTTTATTAATTAATTAATTAATTAATTTTAA 136193
1447 TTATGAGCTAAGTACTTATTTATGTTTATTAATTTGAATGCTTTTAAGTTACA 1506

Dd 136192 ATATATAATATTATTTATATATCTAATATAATATATATATATTATATATTTTA 136133

Dy 1507 TAAAAATTCGAATTAGTTTTAAAAAAA 1537
||||| - ||||| - ||||| - |||||
Db 136132 TAAATATATAAATATATTTTAACTATAAAAA 136102

RESULT 6

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US-11-155-492-1/c
Sequence 1, Application US/11155492
Publication No. US20050266479A1
GENERAL INFORMATION:
APPLICANT: Weissenbach, Jean
APPLICANT: Hazan, Jamil
TITLE OF INVENTION: CLONING, EXPRESSION AND CHARACTERIZATION OF THE SPQ4
TITLE OF INVENTION: GENE RESPONSIBLE FOR THE MOST COMMON FORM OF AUTOSOMAL
TITLE OF INVENTION: DOMINANT SPASTIC PARAPLEGIA
FILE REFERENCE: R-341894
CURRENT APPLICATION NUMBER: US/11/155,492
CURRENT FILING DATE: 2005-06-20
PRIOR APPLICATION NUMBER: US/09/830,902
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: FR 93 11097
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: PCT/FR00/02433
PRIOR FILING DATE: 2000-09-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Vers. 2.0
SEQ ID NO 1
LENGTH: 110000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: exon
LOCATION: (9932)...(10471)
FEATURE:
NAME/KEY: intron
LOCATION: (10472)...(33718)
FEATURE:
NAME/KEY: exon
LOCATION: (33719)...(33805)
FEATURE:
NAME/KEY: intron
LOCATION: (33806)...(35748)
FEATURE:
NAME/KEY: exon
LOCATION: (35749)...(35832)
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NAME/KEY: intron
LOCATION: (35833)...(45022)
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NAME/KEY: exon
LOCATION: (45023)...(45118)
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NAME/KEY: intron
LOCATION: (45119)...(60863)
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NAME/KEY: exon
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NAME/KEY: intron
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NAME/KEY: exon
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NAME/KEY: intron

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LOCATION:	(62439)...	(73173)
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NAME/KEY:	intron	
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NAME/KEY:	intron	
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NAME/KEY:	exon	
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NAME/KEY:	intron	
LOCATION:	(91234)...	(93443)
FEATURE:		
NAME/KEY:	exon	
LOCATION:	(93444)...	(93484)
FEATURE:		
NAME/KEY:	intron	
LOCATION:	(93485)...	(100599)
FEATURE:		
NAME/KEY:	exon	
LOCATION:	(100600)...	(102009)
US-11-155-492-1		

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Best Local Similarity	56.2%	Pred. No. 2.8		
Matches 82	Conservative	0	Mismatches 64	Indels 0
			Gaps	0

Oy	1392	TAAATTTTCAATGTTTTTAATTTTAAAAATTCTAATTTACTGCACATTTATG	1451
Db	107003	TAAATTAATCTGAATATAATTAATTCATTTTAGCCCTCTGACCCTCATGGTATTTCTGT	106944
Oy	1452	GGACTAGTACTCTTTTATTAAGTTTATTAATTGGAATGTGTTTTAACTTAACTATAAAA	1511
Db	106943	CCTAATTTTACTATACATTAATTAATTAATTAACAACCTGCACATTAATTTTGTGTGCTTTAAA	106898
Oy	1512	TTGCCAATTAGTTTTAAAAAAAAAAAAA	1537

	Query Match	2.8%	Score 43	DB 6	Length 98716
	Best Local Similarity	54.8%	Pred. No. 3.8		
	Matches 85	Conservative 0	Mismatches 70	Indels 0	Gaps 0
QY	1379 TGAATTGATGATATATTTTCACACGTTTATATTTTATATAATTTACTAAATTTAC				1438
DB	18403 TTAATTATTAATTAATTAATTTTAAATAATTAATTAATAATTAATTAATTAAT				18463
QY	1439 ATGACAAATTTATGGACCACTACTATTATATGTTTATATATTTGAATAGCTGTTT				1498
DB	18463 TTTATATATTTTATTTTAAATATATTTTAAATAATTTATTTTAAATATATATTTT				18522

Query Match	2.8%	Score 42.4	DB 6	Length 2901
Best Local Similarity	58.9%	Pred. No. 0.68		
Matches 73; Conservative	0	Mismatches	51	Indels 0
				Gaps 0


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Oy      1383  TTGGATTGATTAATATTTCATCATGTTTATATTTTATAAAATTTTCTAATATTACATGA 1442
Db      1580  TTTTATTATTAAGCTTCATTAATATTTTCTATATTAATTATTAATATGTAACGTTACCTGC 1649
Oy      1443  CAATTATGAGCACTAAGTTACTTATTTATATATGTTTATATATATTTGAAATGTGTTTAAGT 1502
Db      1650  TAAATTAATTAATCTCATTTTGATATCCAAATCTGTGCTTATGATATGCTTCTTAGT 1709
Oy      1503  TACA 1506
Db      1710  AAAA 1713

RESULT 11
US-11-121-086-25
: Sequence 25, Application US/11121086
: Publication No. US20050266459A1
: GENERAL INFORMATION:
: APPLICANT: FOULSEN, TIM S.
: APPLICANT: NIELSEN, KRISTEN V.
: TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
: FILE REFERENCE: 09138, 6000-00000
: CURRENT APPLICATION NUMBER: US/11/121, 086
: CURRENT FILING DATE: 2005-05-04
: PRIOR APPLICATION NUMBER: 60/567, 570
: PRIOR FILING DATE: 2004-05-04
: NUMBER OF SEQ ID NOS: 107
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 25
: LENGTH: 173602
: TYPE: DNA
: ORGANISM: Homo sapiens
US-11-121-086-25

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[illegible]

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; TYPE: DNA
; ORGANISM: Bovine 19866881301738
US-10-750-185-64246

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Query Match 2.7%; Score 42; DB 6; Length 1659;
Best Local Similarity 51.6%; Pred. No. 0.62;
Matches 96; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy	1351	TGGCTCCCTCGAGAAAGATCTCACTCCTCGAATTTGGATATGATTAATTAATCAATGTTT	1418
Db	1559	TGAATATTCATAACACAATTTTACTGATCTAATAAGAGAACATTAATATATGAAATTA	1500
Qy	1411	ATAATTTTATAAATTTTACTAAATTTACATGACAAATTAATGGACTAAGTTACTATTTA	1470
Db	1499	TTTTTTTTATAATTTTGCAGAGATATTCATGCAAAATTAATTAATCTCAAGCCGATCTT	1448
Qy	1471	TATGTTTATTAATATTTGAAATGCTTTTAAGTACATTAATAATTCGAATTAAGTTTAAAA	1533
Db	1439	TATAGCAATATTTCCGATTTTATTAATTTCAATATAATCAAAATATCAATCTTTTAACATA	1380
Qy	1531	AAAAAA	1536
Db	1379	CACATA	1374

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RESULT 13
US-10-750-185-46813
Sequence 46813, Application US/10750185
Publication No. US2005026063A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Denis
TITLE OR INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US-60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46813
LENGTH: 4063
TYPE: DNA
ORGANISM: Bovine
US-10-750-185-46813
19866881028899

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Query Match	2.7%	Score 41.8;	DB 6;	Length 4063;
Best Local Similarity	55.0%	Pred. No. 1.2;		
Matches	82;	Conservative	0;	Mismatches 67;
			Indels	0;
			Gaps	0;

Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db		
1382	ATTGATGGTAAATATTCATCAGTTTTATTTATATAATTTCTAAATTACAG	1441	ATTGATGGTAAATATTCATCAGTTTTATTTATATAATTTCTAAATTACAG	1442	ACAAATTATGGGACTAGTACTATTTATATGTGTTATATATTGAAATGCTTTAG	1501	ACAAATTATGGGACTAGTACTATTTATATGTGTTATATATTGAAATGCTTTAG	1502	TTACATATAAATTCGCAATTAGTTTTAAADA	1530	TTACATATAAATTCGCAATTAGTTTTAAADA
2389	ATTGGTACATAAATAAATGTCATTATTTATACAAATGACAAATAAATTGTAT	2448	ATTGGTACATAAATAAATGTCATTATTTATACAAATGACAAATAAATTGTAT	2449	CTATGGTATGCTATATATGCTATGTCATCGTAGATATATAACAAAGACTTGTTTTATA	2508	CTATGGTATGCTATATATGCTATGTCATCGTAGATATATAACAAAGACTTGTTTTATA	2509	TTGCATACAAATTTAAAAACAGTTTTTTTAAA	2537	TTGCATACAAATTTAAAAACAGTTTTTTTAAA

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RESULT 14
US-10-995-561-13235
; Sequence 13235, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: December 26, 2005, 08:04:27 ; Search time 1348.14 Seconds
(without alignments)
9427.811 Million cell updates/sec

Title: US-10-674-540A-1

Perfect score: 1537
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	100.0	1537	US-10-674-540-1	Sequence 1, Appli
2	448	29.1	1900	US-10-424-599-10323	Sequence 10323, A
3	351.4	22.9	1239	US-09-938-842A-2482	Sequence 2482, Ap
4	351.4	22.9	1239	US-09-938-842A-2482	Sequence 2482, Ap
5	291.2	18.9	1167	US-10-674-540-15	Sequence 15, Appl
6	165.6	10.8	2199	US-10-437-963-60348	Sequence 60348, A
7	154	10.0	1340	US-10-437-963-911	Sequence 911, App
8	152.4	9.9	778	US-10-767-701-23	Sequence 23, Appl
9	151	9.8	1384	US-10-425-114-1427	Sequence 1427, A
10	151	9.8	1384	US-10-425-115-105259	Sequence 105259, A
11	139.4	9.1	786	US-10-425-115-55840	Sequence 55840, A
12	133	8.7	464	US-10-767-701-28008	Sequence 28008, A
13	131.8	8.6	923	US-10-674-540-6	Sequence 6, Appli
14	124.6	8.1	588	US-10-424-599-43547	Sequence 43547, A
15	117.6	7.7	1481	US-10-437-963-13102	Sequence 13102, A
16	112.6	7.3	1481	US-10-425-115-21097	Sequence 21097, A
17	110.4	7.2	1812	US-10-437-963-47718	Sequence 47718, A
18	109.6	7.1	594	US-10-260-238-5250	Sequence 5250, Ap
19	107.4	7.0	2812	US-10-437-963-36187	Sequence 36187, A
20	105.6	6.9	2043	US-10-425-114-32590	Sequence 32590, A
21	105.6	6.9	2138	US-10-425-115-159545	Sequence 159545, A
22	104.6	6.8	1543	US-10-437-963-36545	Sequence 36545, A
23	101.4	6.6	1417	US-10-739-930-506	Sequence 506, App

C 24	98.4	6.4	1589	8	US-10-739-930-4239	Sequence 4239, Ap
C 25	98.2	6.4	2812	7	US-10-437-963-36187	Sequence 36187, A
C 26	97	6.3	1257	7	US-10-437-963-50552	Sequence 50552, A
C 27	93	6.1	1576	7	US-10-425-114-23226	Sequence 23226, A
C 28	93	6.1	1596	8	US-10-425-115-103597	Sequence 103597, A
C 29	92	6.0	1522	7	US-10-425-114-15537	Sequence 15537, A
C 30	92	6.0	2008	7	US-10-425-114-17036	Sequence 17036, A
C 31	92	6.0	2153	8	US-10-425-115-65837	Sequence 65837, A
C 32	91	5.9	1591	7	US-10-425-114-2476	Sequence 2476, Ap
C 33	90.4	5.9	1878	7	US-10-425-114-22850	Sequence 22850, A
C 34	90.4	5.9	1913	8	US-10-425-115-65835	Sequence 65835, A
C 35	90.4	5.9	1927	7	US-10-425-114-15565	Sequence 15565, A
C 36	90.2	5.9	688	7	US-10-767-701-7110	Sequence 7110, Ap
C 37	88.2	5.7	640	7	US-10-767-701-4765	Sequence 4765, Ap
C 38	85.4	5.6	1536	7	US-10-425-114-10975	Sequence 10975, A
C 39	85.4	5.6	1627	7	US-10-425-114-12392	Sequence 12392, A
C 40	85.4	5.6	1784	7	US-10-424-599-12392	Sequence 12392, A
C 41	79	5.1	552	7	US-10-437-963-36185	Sequence 36185, A
C 42	77	5.0	1518	7	US-10-425-114-4612	Sequence 4612, Ap
C 43	76.8	5.0	1641	7	US-10-425-114-10888	Sequence 10888, A
C 44	75.8	4.9	2014	7	US-10-424-599-48229	Sequence 48229, A
C 45	72.2	4.7	900	8	US-10-425-115-14816	Sequence 14816, A

ALIGNMENTS

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RESULT 1
US-10-674-540-1
; Sequence 1, Application US/10674540
; Publication No. US20040156891A1
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE.
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/10/674, 540
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 09/597, 774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250, 280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105, 815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1537
; TYPE: DNA
; ORGANISM: Plant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (48)...(1390)
US-10-674-540-1

Query Match      100.0%; Score 1537; DB 7; Length 1537;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCACGAGCATTCCTCAAAATCTCTTACGACGCTCAAAATCTTCAACATGAGGCTGCAATG 60
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DB      1  GCACGAGCATTCCTCAAAATCTCTTACGACGCTCAAAATCTTCAACATGAGGCTGCAATG 60

QY      61  CCNAACCTTTAGGCTCTCAAAAGCCGCCCAACATGAGGCTGCGGTCATG 120
      |||
DB      61  CCNAACCTTTAGGCTCTCAAAAGCCGCCCAACATGAGGCTGCGGTCATG 120

QY      121  CTTGGGCGGGGCTACTTAAACCGCTCAACGATGAGCTCGTGAGCTCTCTTACGCTGCG 180
      |||
DB      121  CTTGGGCGGGGCTACTTAAACCGCTCAACGATGAGCTCGTGAGCTCTCTTACGCTGCG 180

QY      181  GGAGCTTCTCGCAGGTGATAGACACTTCAATTAAGACAGAACTGCTCTTACGCG 240
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Db 181 GGGACTTCGCGAGTGACATACGACACTTCATPAAGCACAAGAACTGCTCTATGCG 240
Qy 241 GCACAGACCCGTAGGGAGGCGGACCTTCACTTAACACGCCCTTCCCGGGGGCGGAG 300
Db 241 GCACAGACCCGTAGGGAGGCGGACCTTCACTTAAAGCCCTTCCCGGGGGCGGAG 300
Qy 301 ACCGGTTGACGTGTGGCGCTTCTTGTACGCCCACTCGAAGGTGAGCGCTCCAGAGCGT 360
Db 301 ACCGGTTGACGTGTGGCGCTTCTTGTACGCCCACTCGAAGGTGAGCGCTCCAGAGCGT 360
Qy 361 TTCTGCTGAAGTCGAGGTGAGGAGAAAGTGAGATGAGGAATCGAATTGATTTGGATG 420
Db 361 TTCTGCTGAAGTCGAGGTGAGGAGAAAGTGAGATGAGGAATCGAATTGATTTGGATG 420
Qy 421 TCGGTGTCTCGAATGACGACGAGCTGGGTGGCGGAGCGAAGGAGGTGTATGGGTGT 480
Db 421 TCGGTGTCTCGAATGACGAGCTGGGTGGCGGAGCGAAGGAGGTGTATGGGTGT 480
Qy 481 GGAGAGGGACTTGTAGGGAATATGAGTGGGTGATGTTCTTGTGCTCAACTTGAGTCTG 540
Db 481 GGAGAGGGACTTGTAGGGAATATGAGTGGGTGATGTTCTTGTGCTCAACTTGAGTCTG 540
Qy 541 CTCACTCTTGTGTACGCACTCAACAACTACTCATGTTGAAAAGGTGAAAATGAGAAA 600
Db 541 CTCACTCTTGTGTACGCACTCAACAACTACTCATGTTGAAAAGGTGAAAATGAGAAA 600
Qy 601 AGAAGAGATTCATPAATCAAGTTGCTGACGCTGTTTCAATATCAACCTACTAGTTCCG 660
Db 601 AGAAGAGATTCATPAATCAAGTTGCTGACGCTGTTTCAATATCAACCTACTAGTTCCG 660
Qy 661 CGTCCAAAGACAAAGAAAGAAAGGAGCGACGACGATGATGACGACCCCAAGTATGC 720
Db 661 CGTCCAAAGACAAAGAAAGAAAGGAGCGACGACGATGATGACGACCCCAAGTATGC 720
Qy 721 AAGGTGGATGACATATATACATCGAGAGATCCCAATCAACCTTCAAAAATAAGTG 780
Db 721 AAGGTGGATGACATATATACATCGAGAGATCCCAATCAACCTTCAAAAATAAGTG 780
Qy 781 CAAGAACCAACTTCAACCACTCAACCACTCAACCACTCAACCACTCAACCACTCAAC 840
Db 781 CAAGAACCAACTTCAACCACTCAACCACTCAACCACTCAACCACTCAACCACTCAAC 840
Qy 841 TAAAGATTAACATTCGCGGTGACAGCTTACAGCGGACGACCTATCACTGCGCTTCCG 900
Db 841 TAAAGATTAACATTCGCGGTGACAGCTTACAGCGGACGACCTATCACTGCGCTTCCG 900
Qy 901 ACATAGTGAAGATCTCAACGACGAGATCCAGTCAAGCGCGGTGCTTGGGTGCCAA 960
Db 901 ACATAGTGAAGATCTCAACGACGAGATCCAGTCAAGCGCGGTGCTTGGGTGCCAA 960
Qy 961 AAGTAGGCAACAAAAATTCACAACTCTTCACTGACCTCAACCTTAATATGCTTCC 1020
Db 961 AAGTAGGCAACAAAAATTCACAACTCTTCACTGACCTCAACCTTAATATGCTTCC 1020
Qy 1021 ATGTAAGGAATGTCACTGACCTGATCCCTGTATCCCGTGAAATCTCATGGGTACGTA 1080
Db 1021 ATGTAAGGAATGTCACTGACCTGATCCCTGTATCCCGTGAAATCTCATGGGTACGTA 1080
Qy 1081 ACATAGGAATGTCACTGACCTGATCCCTGATCCCGTGAAATCTCATGGGTACGTA 1140
Db 1081 ACATAGGAATGTCACTGACCTGATCCCTGATCCCGTGAAATCTCATGGGTACGTA 1140
Qy 1141 ACCGAGGTATGGCATATTTGCAAGCAATTTGCAATGTTGAAGGTGTTGGATGGGG 1200
Db 1141 ACCGAGGTATGGCATATTTGCAAGCAATTTGCAATGTTGAAGGTGTTGGATGGGG 1200
Qy 1201 TTAAGGGGAGTTTAAGGTGTAATTAAGAGAGGTGCAATGGTGTATTAAGTATG 1260
Db 1201 TTAAGGGGAGTTTAAGGTGTAATTAAGAGAGGTGCAATGGTGTATTAAGTATG 1260
Qy 1261 ATTTCTTAAGAGAAATGTTGTTCTCCAGCTTGTGGTTGTGCAACAAAGGA 1320
Db 1261 ATTTCTTAAGAGAAATGTTGTTCTCCAGCTTGTGGTTGTGCAACAAAGGA 1320
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Db 1261 ATTTCTTAAGAGAAATGTTGTTCTCCAGCTTGTGGTTGTGCAACAAAGGA 1320
Qy 1321 TGGTTTGAATTAAGAGATGAGTGGGTGTTGGCTCTCTCGAGGAAGATCTACTCTG 1380
Db 1321 TGGTTTGAATTAAGAGATGAGTGGGTGTTGGCTCTCTCGAGGAAGATCTACTCTG 1380
Qy 1381 AATTGATGATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1440
Db 1381 AATTGATGATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1440
Qy 1441 GACAAATTAAGGACCTAAGTACTTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
Db 1441 GACAAATTAAGGACCTAAGTACTTAATTAATTAATTAATTAATTAATTAATTAATTA 1500
Qy 1501 GTTACATPAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1537
Db 1501 GTTACATPAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1537

RESULT 2
US-10-424-599-10323
; Sequence 10323, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ. ID NOS: 285684
; SEQ. ID NO 10323
; LENGTH: 1900
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_109323C.1
US-10-424-599-10323

Query Match 29.1%; Score 448; DB 7; Length 1900;
Best Local Similarity 59.4%; Pred. No. 1,2e-95;
Matches 862; Conservative 0; Mismatches 510; Indels 78; Gaps 3;

Qy 85 CCGGCCCAACATGCGCCGAATCTCTCGGATCCATGCTTTGGCCGCGGCTACTAAACCCGC 144
Db 418 CGAGGCCCAAGTGGCCGAGCTCTGCGCGCGCAACCTGCGCGGCTACTAGACCTTC 477
Qy 145 TCAACGATGAGCTCGTAGGCTCTCTCAAGCTGCGGGGACTTCTGCGCAAGTACATACG 204
Db 478 TCCACCCCTCTCTCGCTCTCTGATCTCTCGGTGCGGGGACTATCAAGCCACTACG 537
Qy 205 ACACCTTCATPAACGACAGAACTGCTCTAATGCGGACAGCGCTTACGGAAGCGG 264
Db 538 ACGCTTCAACAAAGACAGAACTGCTCTAATGCGGACAGCGCTTACGGAAGCGG 597
Qy 265 ACCTACTTCATPAACGCGCTCTCCGCGGGGCGGACGCGGTTGAAGTGTGGCGTA 324
Db 598 CTTTCTTCCGAG--GTAAGTGTGAGCTGCCCGAGAAATTAAGAGTGGCGGCTTCC 654
Qy 325 TGTAGCGCATGCGAAGGTGACGCTGCCAGAGGCGTTTGTGCTGAATGCGAGTCCGAGG 384
Db 655 TCTATGCCACCGCAAGGATCACGCTCCGAGGCTTCTCTCTCACTCGCTCGCGCG 714
Qy 385 AGAAGTGGATTAAGGAAATGCAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 444
Db 715 AGGCTGGGACCGGAGTCCAACTGATTTGCTATTCGCGCTCAATCAGATCGCGAT 774
Qy 445 GTCCGGTGGCGGACGAAAGGAGTGTATGTTGTGTGAAGAGGACTTTGAGGATTA 504
Db 775 CCCAAGAACTCGGAGGAGGAGATCTACGTGTGTGAGAGGAGCAACAGGAGCAATGG 834
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505 AGTGGTGTGATGTTCTTGGTGTCACTTGAAGTCTGATCCTTTGTTAGCACTCAAC 564
565 AAATCTACTGATGTTGAAAAGGTGAAAATGAGAAAAGAAAGCAATTCATTAATCAAGTT 624
895 GCTCTAAAGAGCTGAAGATGAAAACAAAGACGGTAGAGACGACGAGTGA----- 946
625 GGTACGACTGTTTCAATATCAACCTAATAGGTTCCGCGTCCAAAGACAAAGAAAAGAA 684
947 ----- 946
685 GCGACGACGATGATGACGACCCCAAGATGATGCAAGTTGATGACATATACACAT 744
947 -CGAGAGACGACCCGAGAAAACGAGAGTATGTCGGGTGGCTCAACATCTACACGT 1005
745 CGAGAGATCCCAATCAACCTTCAACAACTAAGTGAAGAACCAACTTCAGACCAAC 804
1006 CTGACACCCCAAAATCCCTTTACCAAAATCAGGAGCAAGAACGAGCTTCAAGCCACG 1065
805 TCACAACTATATGACAAATACAAAGACGAAACCTTAAGCATTAATTCGCGGTACA 864
1066 TCAATCTCTTCAACATTACAGCTCTGAGAACCCGAGCTTGTCAATCGTGGGGCACA 1125
865 GCGTAGGGGCGACATATCACTGAGAGCGCTTCAAGTGAAGATCTCAACGACG 924
1126 GCGTGGGCGAACCTTATCAATCGAGAGCGCTTCAAGTGAAGATCTCAACGAGG 1185
925 AGATCCGAGTCAAGCGCGTGTCTTGGGTCGCCCAAGTGAAGCAAAATTTCCAC 984
1186 AGGTCCGAGTCAAGCGCGTGTCTTGGGTCGCCCAAGTGAAGCAAAATTTCCAC 1245
985 AACTCTTGAATCTGATCCCAACCTAAATGTCCTCATGTAAGAGATCTCATCTGA 1044
1246 AGAGTTTCAACATGTTTCCGAACCTTGAAGTGTGCAAGTGAAGCACTGATTCATTTGA 1305
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1306 TCCCACTACCCGAGAGTGTGTTAGGATGATGATGATGATGATGATGATGATGATG 1365
1105 ACTGAGAGAGTCAACCTTTCTAAAGACCTGAAACCCGAGTGAATGATGATGATG 1164
1366 ACAGAGAGAGTCCGCGGAGCTTGAAGAGTGAAGAGTCCGCGGTGATGATGATGATG 1425
1165 AAGCAATGTCATGTTGTAAGTGTGATGATGATGATGATGATGATGATGATGATG 1224
1426 AAGCAATGTCATGTTGTAAGTGTGATGATGATGATGATGATGATGATGATGATG 1485
1225 ATAGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1284
1486 TGAAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1545
1285 TTCCCTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1344
1546 TCCCAAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1605
1345 GGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1398
1606 GGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1665
1399 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1458
1666 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1725
1459 GTTACTAT 1518
1726 AATCTCTAAT 1785
1519 TAGTTTTTAA 1528
1786 TTATGTTTAA 1795

RESULT 3
US-09-938-842A-2482
Sequence 2482, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPI300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2482
LENGTH: 1239
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-2482
Query Match 22.9%; Score 351.4; DB 3; Length 1239;
Best Local Similarity 57.9%; Pred. No. 8.8e-73;
Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;
89 CCCAACATGCGCCGAACTCTCTCGGAGTCAATGCTTGGGCGGCTACTTAACCGCTCA 148
15 CACATCATGGAAGAACTCTTAGCTCAAGAAATGGGAACTATCTTAGACCATTAAGA 74
149 CGATGACCTCCGAGTCTCTCTAGCTGAGGGAATCTTGCAGAGTGAATACGACAC 208
75 CCATCATCTTAGGAACTCATCTTACGTTGTGGGACCTTTGTCAAGCAGCTACAGTGC 134
209 CTTCTAATACGACCAAGACTGTCCTAATGCGGAGAGCCGCTACGGAAGGCGGACT 268
135 CTTCGACAGACCAAACTCAAGTACTGTGAGCGAGCCGCTACGGAATCTTCTTT 194
269 ACTTCATTAACCGCTTCCCGGGGGCGAGACCGGTTGAAGTGTGAGCTGATCTTGA 328
195 CTTCGACAG---GTCAATGCTCGAAAACGCTTCGACTAGAGGTTGTAACCTTCTCTA 251
329 CGCCACTGCGAAGGTCAAGCTCCAGAGGGGTTCTGCTGAAGTCGAGGTGAGGAGAA 388
252 CGCCAGCTGCTGTGTTCTCTCCCGAAGGTTGCTTCCAAATCAATCAAGAGATTC 311
389 GTGGATAGGAAATCGAATGATGATGATGATGATGATGATGATGATGATGATGATG 448
312 TTGGGACCGGAGATCTAAGTGTGCTACATGCTGATGATGATGATGATGATGATG 371
449 GTGGCGGAGACGAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 508
372 GGCCTTGAAGCGCGTGAAGATCTAATAGCTTGAAGAGGAAACGAGCGGAATCTATG 431
509 GGTGATGATCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 568
432 GGTCAATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 491
569 TACTCATGTTGAAAAGGTGAAAATGAGAAAAGAGAGCATTAATCAAGTTGTA 628
492 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 520
629 CGACTGTTCAATATCAACTACTAGTTCGCGGTCCAAAGACAAAGAAAAGAGAGCA 688
521 CGACTTT-----GATATGTA 536
689 GACGAGATGATGACGACCCCAAGATGATGATGATGATGATGATGATGATGATGATG 748

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Db      537 CAGGAGATGAGAGAGGTGTAGTGTATGCTCGGGGCTCACAATCTATCTCTAA 596
Qy      749 GGATCCCAATCACCCTTTCACAAAACCTAGTGCAGAAACAACTTCAGACCAACAA 808
Db      597 TCACCCCGAATCGAAATTCACCTAGTGAAGTCAAGGCAAGTTGTTAGCAAGATCAA 656
Qy      809 ACACTAATGACAAATACAAAGACGAAACCTTAAGCATTAATTCGCGCGTCAAGCT 868
Db      657 GGACCTCTGTGTAAGTAAAGACGAGAAACGAGCTTGTGTGACTGGACATAGCTT 716
Qy      869 AGGCGGACACTATCACTGCTGAGCGGCTTGCATATGTGAGAA---TTCACGACCGA 925
Db      717 GGGAGCTACAGAGGCTGTTGCGCGCTATGATATAGCTGAGAACGGTTCCAGTATGA 776
Qy      926 GATCCCACTCAGCGCGGCTGCTTCGGGTGCCCAAAAGTAGCAACAAAATTCACA 985
Db      777 TGTTCGGTCACTCTATAGTCTTGTGTTGCCACAGTGAAGAACAGAGTTCAAGGA 836
Qy      986 ACTCTGCACTGTAACCAACTTAATGTCTCCATGTAAAGAAATGTCATGCACTGAT 1045
Db      837 CGAAGTATAGTACAAAGAACTTAAGATCTCTCATTTAAGAAACAGATTTGATCTT 896
Qy      1046 CCTCTGTATCCCGTGAACCTCATGCGTTACGTGAACATAGGAATCGAGTGAATCGA 1105
Db      897 AACTCGATACCCAGGGGACTTTTAGGGTATGTGACATAGGAATTAACCTTTGTGATCGA 956
Qy      1106 CTCGAGGAATCGACCTTCTTAAAGACTCGAAAAACCGGAGTATTTGGCATTTTGA 1165
Db      957 TACAAAGAGTACCGGTTCTTAAGGATTCAGAGATCAAGGAGTTGGCATTAATCTTCA 1016
Qy      1166 AGCAATATGATGTGTATAGTGTGTGATGGGTTAAGGGGAGTTTAAAGTTGTAA 1225
Db      1017 GCGCATGTATATGTGTAGTGTGATGAAATGGAAGAAAGAGTTTAACTGATGCT 1076
Qy      1226 TAAAGAAAGTGTGATTTGTTAATAGTCAATGATTTTCTTAAAGAAAGTTTGT 1285
Db      1077 TAAAGAAAGTATGTCATTAGTGAACAAGTCAATGCAAGTTCTTAAAGCTGAGTTTGT 1136
Qy      1286 TCTTCACACTGTGTGGTGTGTCAGAACAAAGAGATGTTTGAATTAAGATGTGATG 1345
Db      1137 GCCAGAGCTTGTGTGTGTAAGAAACAAAGAGCTGATCAAGAACGAATGTGATG 1196
Qy      1346 GATTTGGCTCCTCTGAGAAAGATCTACTCTGAATT 1384
Db      1197 GGTTCCTCTCCCTTGAAGAAACCTGTACTTAAT 1235

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RESULT 4
US-09-938-842A-2482
; Sequence 2482, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2482
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

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US-09-938-842A-2482
Query Match      22.9%; Score 351.4; DB 3; Length 1239;
Best Local Similarity 57.9%; Pred. No. 8.8e-73;
Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;

Qy      89 CCAACATGGCCCGAATCTCTCGGTCGAATGCTTTGGGCGGGCTACTAAACCGCTCAA 148
Db      15 CACATCATGGGAAAGAACTCTTAGGCTCAAGAAATGGGACACTATCTTAACCATTAAGA 74
Qy      149 CGATGAGCTCCGTAAGGCTCTCCACGCTGCGGGAATTCCTGCAGGTGACATACGACAC 208
Db      75 CCAATCATTAAGGAACTCATCTTACGTTTGGGACTTTTGTCAAGCCACTACGATGC 134
Qy      209 CTTCAATTAACGACAGCAAACTGTCCTACTGCGGACGACGCCGCTACGGAAGGCGACT 268
Db      135 CTTGCTCAAGACCAAACTCAAGTATCTGGAGCCAGCGGATCGGCAAACTTCTTT 194
Qy      269 ACTTCATTAAGACCGCTTCCCGGGGGCGACAGCCGTTTGAAGTGTGCGCTTCTTGA 328
Db      195 CTTGCAAGAG---GTCAATGCTCGAAAACGCTTCGACTAGAGGTTGTAACTTCTCTA 251
Qy      329 CGCCACTCGAAGGTCAAGGCTCCAGAGGGGCTTCTGCTGAAGTCAAGTCAAGTCAAGGAGAA 388
Db      252 CGCCACAGCTGCTGTCTCTCCGAAAGTTGCTTCTCAATCAACAATCAAGAGATTC 311
Qy      389 GTGAGATAGGGAATCGAATTTGATTTGGGTATGTCGTGTGTCGATGCAATGACGAGAGTGC 448
Db      312 TTGGAGACCGTGAAGTCAATGTTTGGCTACATTTGCTGACGCTGATGAACGGTCTAA 371
Qy      449 GTGGCGGAGACGAAGGAGGTGATGTGTGTGAGAGGGACTTTTGGATTATGATG 508
Db      372 GGCCTTTAGGACGCGGTGATGATATATAGCTTTGAGAGGAACGAGCGAATCTATGATG 431
Qy      509 GGTGATGCTCTTGTGTCTCAACTGAGTCTGCTCATCTTTGTTAGCACTCAACAAC 568
Db      432 GGTCAATGTTTGTGTCTAGGCACTTACGTCAGCCCTTGTGACGAGCCGAGCA 491
Qy      569 TACTCATGTTGAAAAGGTGAAAATGAGAAAAGAGATTCATTAATCAACTTGTGA 628
Db      492 GATGCTTCTGTGTGTGATGA---GATA 520
Qy      629 CGACTGTTTCATATTCACCTACTAGGTCGCGCTCCAAAGACAAAGAAAAGAACGA 688
Db      521 GCACTTTT-----GATATGA 536
Qy      689 CGAGACAGATATATGACGACCCCAAGATGACAAAGTTGATGCAATATACATCGGA 748
Db      537 CAGTGAAGATGAAGAAAGGTGTAAAGTGTGCTCGGGTGTCAAACTATATCTTAA 596
Qy      749 GGATCCCAATCACCCTTTCACAAAACCTAAGTGAAGAACCAACTTCAGACCAACTCAA 808
Db      597 TCACCCCGAATCGAAATTCACCTAAGTGAAGTCAAGGTGATGTTTAAAGATCAA 656
Qy      809 ACACTAATGACAAATACAAAGACGAAACCTTAAGCATTAATTCGCGCGTCAAGCT 868
Db      657 GGACCTCTGTGTAAGTAAAGACGAGAAACCGAGATGTTGTGACTGGAACATAGCTT 716
Qy      869 AGGCGGACACTATCACTGCTGAGCGGCTTGCATATGTGAGAA---TTCACAGACCGA 925
Db      717 GGGAGCTACAGAGGCTGTTGCGCGCTATGATATAGCTGAAGACGGTTCCAGTATGA 776
Qy      926 GATCCCACTCAGCGCGGCTGCTTCGGGTGCCAAAAGTAGGCAACAAAATTCACA 985
Db      777 TGTTCGGTCACTGCTATAGTCTTGTGTTGCCACAGTGAAGAAACAGAGTTCAAGGA 836
Qy      986 ACTCTGCACTGTAACCAACTTAATGTCTCCATGTAAAGAAATGTCATGCACTGAT 1045
Db      837 CGAAGTATAGTACAAAGAACTTAAGATCTCTCATGTAAAGAAACGATTTGATCTCT 896
Qy      1046 CCTCTGTATCCCGTGAACCTCATGCGTTACGTGAACATAGGAATCGAGCTGAGATGGA 1105
Db      897 AACTCGATACCCAGGGGACTTTTAGGATATGTGACATAGGAATTAACCTTTGTGATGGA 956

```


Qy	894	CCCTTCGACATAGTGGAGAAATCTCAGACCGAG-----ATCCCAATC	935
Db	1369	GCGTTTCGATATGTGTCGTCAACGGCGTGTCCAAAGTCCGCGACGCGCGACATCCCGGTG	1428
Qy	936	ACGGCCGCGATCTTCGGGTGCGCCCAAAAGTAGCAGACAAATAATTCACAACACTCTTGAC	995
Db	1429	ACGCGCGTGTGTTCGGGAGCCCGCAGATCGGGAACCCGAGTTCAAGAAAGCAGTTCCAG	1488
Qy	996	TCGTACCCAAACCTAAATGTCTCTCATGTAAAGAAATGCATGACCTGATCCTCTGTAT	1055
Db	1489	GAGCAGCCCAACTCGCGGGCGGTGCAGTCATGAGAAATGCCGCACTCATCCGCTTAC	1548
Qy	1056	CCCGTGAAACTCATGGGCTTACGTGAACATAGGAATCGAGCTGGAGATCGACTCGAGAA	1115
Db	1549	CCGAGCGGCTCTCTCGGCTACCGCAACGTCCGGAACACCTCCAGGTGCGACTCCAAAG	1608
Qy	1116	TCGACCTTTCTAAAGGACTCGAAAAACCGAGTATGGCATATATTGCAAGCAATATTG	1175
Db	1609	TGCGCCCTACGTGAAGCGAGACACACGAGCCAGGGACTACCAACAACCTGCAGGGGATCCTA	1668
Qy	1176	CATGTTGTAAAGTGTGGCAATGGGGTTAAAGGGGAGTTTAAAGTTTAAATTAAGAGAAGT	1235
Db	1669	CACACGGTGGCCGGCTCGAACGGGAAGAGACGGGAGTTCAAGCTCCAGGTGAAGCGGACG	1728
Qy	1236	GTTGCATTGGTTAATTAAGTCATGTGATTTTCTTAAAGGAAGAAATGTTTGTCTCCAGCT	1295
Db	1729	GTCGGGCTGTGTGAACAAGTCGAGCGGCTTCTCAAGGACAGCAACTGTGCGGAGTCA	1788
Qy	1296	TGTTGGGTTGTGCAGAACAAAGGAGTGGTTTGTAAATTAAGATGTGTAGTGGTTTGGCT	1355
Db	1789	TGTTGGTGTGAAGAGGAACAAAGGACATGTGCTCGGCCAAGAACGGGGAATGGCAGCTCGAG	1848
Qy	1356	CCTCCTGAAGAGA	1369
Db	1849	GCGCCCGCAGAGGA	1862

```

RESULT 7
US-10-437-963-911
; Sequence 911, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 911
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_100828C.1
US-10-437-963-911

```

Query Match 17; Score 154; DB 7; Length 1340;
Best Local Similarity 54.7%; Pred. No. 8, 28-26;
Matches 374; Conservative 0; Mismatches 300; Indels 10; Gaps 3;

QY 688 ACAGCAGCATGATGACGACCCCAAGTATGCAAGTTGATACATATATACATCGG 747
DB 429 AAGGCCAGGCAGTGCATGACCTCTGTGTGATGAGGGGGATGCTCTGTGTGACAC -GATG 487

QY	748	AGATATCCCAATTCACCCCTTTCACAAACCTAAGTGCAGAAACCAACTTCAGACCAACTCA	807
Db	488	CCGATCCCAAGATCTCAGTACATTAACATTAAGCAGAGTGCAGAGATTCAGAGTCTTGAATAGATCA	547
QY	808	AACAACCTAATGACAAATATACAAAGACGAAACCTTAAGCATATTCGCCGCTGCACAGCC	867
Db	548	AACCGCTCCAGATATGTATACGAGCATGAGAGATCAGCATCACCTTAACAGGCCACAGCC	607
QY	868	TAGGCGGCACACTATCACTCGTGAAGCCCTTCGACATATGTGGAGAAATCTACGACCGAGA	927
Db	608	TTGGGGCTGCACCTTGCACCAATCAATGACCTGACATATGTCTCCATGGTTTACAACAMAA	667
QY	928	TC----CCAGTACGCGCCGCTGTCTTCGGGTGCCCAAAAGTAGAGCAACAAAATTTCCAAC	984
Db	668	GCTGTCCAGTGTCTGTCCCTTCGTCTTCGGTACCCAAAGAGTGGGCAACCTGATTTTCAGA	727
QY	985	AACCTTTCGACTCGTACCCAAACCTAAATGTCTTCATGTAAAGAAATGTCAATCATGACCTGA	1044
Db	728	AAGGCTTCGACAGTGCCTCCAGATTTGAAATGTCTCCGATTCGAAACCTCTCTGTATGTGG	787
QY	1045	TCCCTCTGTATCCCGTGAAACATCATGGGTTACGTGAACATAGGAATCGAGCTGAGATGC	1104
Db	788	TTCCAAACTGGCC-----AAACTAGGATTAACGAGATGCTGCGCACAGAGCTGATGATGC	841
QY	1105	ACTCGAGAGATCGACCTTTCTTAAAGCACTCGAAAAACCCGAGTATGTGCATAAATTTGC	1164
Db	842	ATACAGGGAATGACCATACCTGAAGGCCCTCGGAAATCCCTTAACGTGCATGACATGG	901
QY	1165	AAGCAATATTCGACTTTGTGAATGTGTTGGCATGGGCTTAAAGGGGAGTTTAAGCTTTGTAA	1224
Db	902	AGTGTACATCATATGGGGTTGCCCGGAGCGCAGGGGAGCAACGGAAGGTTTCAAGCTGGAGA	961
QY	1225	ATTAAGAGAAGTGTTCATTTGGTTAATATGTCATGTGATTTTCTTAAGGAAAGATGTTTGG	1284
Db	962	TTGATCGAGACATTCCTTTGTGTTAACAAACGAAAGAGCACTGAAGAATGAGTATGCAA	1021
QY	1285	TTCTCTCAGCTTGTGTGGTGTGTGCAGAACAAAGGATGCTTTTGAATTAAGATGCTGAAT	1344
Db	1022	TTCCATCTCTTGTGGGTGTGTGCAGAACAAAGATATGTGTGAAGGACGAGATGTGCGT	1081
QY	1345	GGGTTTTGGCTCTCTCTGAGGAAG	1368
Db	1082	GGCATTGTGGCCGACCATATGAGATG	1105

```

      RESULT 8
      US-10-767-701-23
      / Sequence 23, Application US/10767701
      / Publication No. US20040172684A1
      / GENERAL INFORMATION:
      / APPLICANT: Kovalic, David K.
      / APPLICANT: Zhou, Yihua
      / APPLICANT: Cao, Yongwei
      / TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
      / TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
      / FILE REFERENCE: 38-21(53535)B
      / CURRENT APPLICATION NUMBER: US/10/767,701
      / CURRENT FILING DATE: 2004-01-29
      / NUMBER OF SEQ ID NOS: 63128
      / SEQ ID NO 23
      / LENGTH: 778
      / TYPE: DNA
      / ORGANISM: Sorghum bicolor
      / FEATURE:
      / OTHER INFORMATION: Clone ID: SORBT-28MAY03-CLUS100312_1
      US-10-767-701-23

```

Query Match	9.9%	Score 152.4	DB 7	Length 778
Best Local Similarity	57.5%	Pred. No. 1.5e-25		
Matches 323	Conservative	0	Mismatches 221	Indels 18
			Gaps	2
QY	839	CCTAAGCATACATTGCGCGGTACAGCCTTAAGCCGGAACATATACATGTCGTAGCGCCCTT	898	


```
Db      9  CCTGAGCATCGTGTGCAAGGCGCAAGCCTCGGCGCTGCTGCGCAAGCTTCGCGCTT 68
Qy      899  CGACATAGTGAAGATCTCAGA-----CGAGATCCAGTCAAGCGCCT 943
Db      69  CGACATGCGGTGAACGCGGTGTCCAGGGTGGCGCGCGCCGACATCCCGTACGCGCAT 128
Qy      944  GGTCTTGGGTCGCCCAAAAGTAGGCAACAAAATTCACAACTCTTGACTGTAACC 1003
Db      129  CGTGTTCGGGAGCCCGCAGATTCGGGAACCCGAGTTCAAGAAAGAGTTCCAGAGAGTCC 188
Qy      1004  AAACCTTAATGTCTCCATGTAAAGATGTCAATGACCTGATCCCTGTATCCCGTGA 1063
Db      189  CAACCTGCGGCGCTGCACTGAGGAACCGCCGACCTGATCCCGTGTACCCGAGCG 248
Qy      1064  ACTGAGGGTTACGTGAACATAGGAATCGAGTGTGAGATCGACTCGAGAGTGCAC--- 1120
Db      249  CCTCTGGGCTTACGCAACGCGCGGAGCTCTGCGCTGAGCTCCAAAGAGTGCCTGA 308
Qy      1121  CTTTCTAAAGACTCGAATAAACCCGAGTATGTCATATTGCAAGCAATATTGCAATGT 1180
Db      309  CGTGAAGAAGACCTTCACCAACCTCGGGGACTACCAACCTGCAAGGCACTCTGCACAC 368
Qy      1181  TGTAAAGTGTGGCATGAGGAGTTAAAGGGAGTTTAAAGTTAAATTAAGAAAGTGTTC 1240
Db      369  GGTGCGGGCTGGAACGGCAAGACGCGGAGTTCAAGCTGCAAGGTGCAGCGCAGCTGGC 428
Qy      1241  ATTGGTTAATAGTCACTGATTTTCTTAAGGAAGATGTTTGTCTCTCAAGTGTGTG 1300
Db      429  GCTGTGAACAAAGTGTCTCGGCTTCCTCAAGGACGACAACTCGTCCGAGATGATGTG 488
Qy      1301  GGTGTGTCAGAACAAAGGATGTTTGAATTAAGATGATGATGTTGGTCTCTCC 1360
Db      489  GGTGAAGCGGAACAAAGGAGATGTCATCGAGAAACCGGCGTGTGGAGCTCGAGCTCC 548
Qy      1361  TGAGGAAGATCTACTCTCTGAA 1382
Db      549  TGCCGAGGAAGAACCTTCCCGTA 570

RESULT 9
US-10-425-114-31427
; Sequence 31427, Application US/10425114
; Publication No. US2004003488BA1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425.114
; NUMBER FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31427
; LENGTH: 1384
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73170B05_FLI
US-10-425-114-31427
```

Query Match 9.8%; Score 151; DB 7; Length 1384;
Best Local Similarity 53.8%; Pred. No. 4.3e-25;
Matches 363; Conservative 0; Mismatches 300; Indels 12; Gaps 2;

```
Qy      702  GACGACCCCAAGATGATGCAAGTTGATGATGATATATACATATGAGAGATCCCAATCA 761
Db      556  GCCAACCCCTGTGTGATGATGAGGAGGCTTTCAGTCTACAGAGTGTGATCCAGGAGCA 615
Qy      762  CCTTCACAAAAGTAAAGTGAAGAACAACTTCAAGACCAAACTCAAACTAATATGACA 821
```

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Db      616  CAGTACAAACAAAGAGACGGCAAGCATCAGTGTTAACAGAGGTGAAGAAAGATACAGAT 675
Qy      822  AAATACAAAGCAAAACCTTAAGATTAACATTCGCCCGGTGACACCTTACAGGCGCACTA 881
Db      676  CTGTAAAGCCAGAGGAGACAGAGATCACTAAACAGCCACAGCTTAAAGGAGCACTT 735
Qy      882  TCACTGTGAGCGCTTCGACATAGT-----GAGAAATCTCAAGCCGAGATCCCAATC 935
Db      736  GCCACATCAACGCAACCGACATGTCTCCAAAGGCTTCAACAGAGAGCTGTGCTGTG 795
Qy      936  ACGGCGGTGTCTTCGAGTGTCCCAAAAGTAGCAACAAAATTCACAACTCTTCGAC 995
Db      796  TCGCGTTTGATTCGGGAGGCCAGAGTGGAAACCTTGATTTCCAGAAAGCGCTTCGAC 855
Qy      996  TCGTACCAAACTTAATGTCTCATATGAAGAAATGATCATGACCTGATCCCTGTGAT 1055
Db      856  AGCGGCGGAGCTGAGGCTGCTCCGCTCGGAACTCTCCGAGTGTGTCCTCAAAATGG 915
Qy      1056  CCCGTAAACTCATGGGTTACGTGAACATAGAAATCGAGTGTGAGATCGACTCGAGAA 1115
Db      916  CCAAG-----CTAGGTACAGATGATGTGCGCACAGACTGATGATCGACAGAGAA 969
Qy      1116  TCGACCTTTCTAAAGACTCGAATAAACCCGAGTATGCAATATTGCAAGCAATATTG 1175
Db      970  TCGCGTACCTGAAGGCCCTCGAAGACCCCTGACATGAGATGATGATGCTGATCATG 1029
Qy      1176  CATGTGTAAAGTGTGTCATGAGGAGTTAAAGGGAGATTTAAAGTTGAATTAAGAAAGT 1235
Db      1030  CACGGGTCGCTGTGGGCTCAGGGGAGCAGCGGAGGTTGCGTGTGTGATCGAGGAC 1089
Qy      1236  GTTCATTTGTTAATAGTCAATGATTTTCTTAAGGAAGATGTTGTTCTCTCAAGT 1295
Db      1090  GTTGCTTTGTTGAACAGATGAATGATGCTTGAAATGATGTTGCTGCTCCACCGTGC 1149
Qy      1296  TGTGAGTGTGTGCAACAAAGGATGTTTGAATTAAGATGATGATGATGATGATGATGCT 1355
Db      1150  TGTGAGTGTGTGCAACAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1209
Qy      1356  CCTCTGAGGAAGT 1370
Db      1210  GACCATGAGGAGGAT 1224

RESULT 10
US-10-425-115-105259
; Sequence 105259, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425.115
; NUMBER FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 105259
; LENGTH: 1384
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_27497C.1
US-10-425-115-105259
```

Query Match 9.8%; Score 151; DB 8; Length 1384;
Best Local Similarity 53.8%; Pred. No. 4.3e-25;
Matches 363; Conservative 0; Mismatches 300; Indels 12; Gaps 2;

```
Qy      702  GACGACCCCAAGATGATGCAAGTTGATGATGATATATACATATGAGAGATCCCAATCA 761
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Db 556 GCCAACCCCTGTGTGATGAGAGGTGCTTTCAGTCTACACGAGTGTGATCCAGGGTCA 615
Qy 762 CCCCTTCAAAACCTAAGTGAAGAACAACAATCTGACACCAACTCAACATCAATATGACA 821
Db 616 CAGTACAAACAAAGAGCGCAAGACATAGGTGTTAAACGAGTGAAGAAAGGATCAGGAT 675
Qy 822 AAATACAAAGACGAACCCCTAAGCATTAATTCGCGGTGACAGCTTAGCGCGACATA 881
Db 676 CTGTACAAAGCAGAGAGAGAGCATCATTAACAGCGCACAGCTTAGAGAGCACTT 735
Qy 882 TCACTGTAGCGCTTGTGACATAGT-----GGAAATCTCAGACCGAGATCCAGATC 935
Db 736 GCCACATCAACGCAACCGACATGCTCTCAACGCGCTACCAACAGAGCTGTGCTGTGTG 795
Qy 936 AGCGCGGTGTCTTGGGTGCGCAAAAGTAGGCAACAAAATTCACCAACATCTTGGAC 995
Db 796 TCCCGCTTGTATTCGGAGAGCCAGAGTCCGAAACCTTGAATTTCCAGAGCGCTTGAC 855
Qy 996 TCGTACCCAAACCTAATATGCTCTCATGTGAAGATGATGATCGACTGATCCCTGTAT 1055
Db 856 AGCGCGCGGACCTGAGGCTCTCCGCTCCGGAACCTCCGACGTGTCTCCCAATGG 915
Qy 1056 CCCGTAACTCATGAGGTGATAGTGAACATAGGAATCGAGCTGAGATGACTCGAGAG 1115
Db 916 CCAAG-----CTAGGGGTACATGATGTCCGACACAGAGCTGATGATGACACAGAGAA 969
Qy 1116 TCGACCTTTCTAAGGATCTCGAAAACCGGATGATGGCATTAATTCAGCAATATTTG 1175
Db 970 TCGCGTACCTGAAGGCTCCCTGGAACCCCTGACATGACATGATGATGATGATGATG 1029
Qy 1176 CATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1235
Db 1030 CACGGGCTCGCTGGGGCTCAAGGGGAGCAGCGAGGCTTGAAGCTGTGTGTGTGTGTG 1089
Qy 1236 GTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1295
Db 1090 GTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1149
Qy 1296 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1355
Db 1150 TGTGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1209
Qy 1356 CTTCTGAGGAAGAT 1370
Db 1210 GACCATGAGGAGAT 1224

RESULT 11
US-10-425-115-55840
; Sequence 55840, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 55840
; LENGTH: 786
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_150920C.1
US-10-425-115-55840

Query Match 9.1%; Score 139.4; DB 8; Length 786;
Best Local Similarity 57.6%; Pred. No. 1.8e-22;
Matches 270; Conservative 0; Mismatches 196; Indels 3; Gaps 1;

Qy 70 TAGGCTCTCAAAAGCCCGCCCAACATGAGCCGAACTCTTGGGTTCATATGCTTGGCCG 129
Db 163 TCGGCGGCGCCAAAGGCTCCGCGCATAGGCGGAGCTGTGCTCCGCGCACTGGAGG 222
Qy 130 GGTACTTAAACCCGCTCAAGATAGGCTCCGTAGATCTCTTCAAGCTTGGGGGACCTT 189
Db 223 GCTCTCTGATTCCTTCAAGCTCAAGCTCCGCGCTCATCTGTGCTGGGCGACCTT 282
Qy 190 GCCAGGTGATATGACACCTTCAATAAAGACCAAGAACTGTCTTACTGCGGAGACCC 249
Db 283 GCCAGGTGATATGATTCCTTCAATCTCAAGCTCAAGCTCAAGTATGATGAGCTGCC 342
Qy 250 GCTACGGAAGGCGGACCTTATTAAGACCGCTTCCGCGGAGGCGCAGACCGTTTG 309
Db 343 GCTACTCAGATTCACGCTCTTCCGCGCAGCTGTTCGCGCGCGCGCAGACATCTT-- 400
Qy 310 AGTGTGTGGGTACTTGTATGACCACTGCGGAAGTCAAGCTCCAGAGCGCTTCTGTGA 369
Db 401 -CCGCGCGGCTACTCTTACGCAACCTCCAGTCTGTTCAGAGCGGTATCATGATGT 459
Qy 370 AGTGAAGTCAAGGAGATGAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 429
Db 460 TCTGCTCTCCGCGAGCGGTGAAACAGAGTCAACTGATGCTTACGTCTCCGTGT 519
Qy 430 CGAATGACAGACGATCGGCTGCGGAGCAGAAAGAGGTATGTGTGTGAGAGGGA 489
Db 520 CCAAGACGCGCGCGCGCGCGCCACGCGCGCAGCGCTCATCTACGTGCGCGCGGCA 579
Qy 490 CTGTAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 538
Db 580 CCATCCGAGCGCTGAGTGGTGTGACGTGTCAAGCCGAGCTGTCTC 628

RESULT 12
US-10-767-701-28008
; Sequence 28008, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 28008
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 7534916
US-10-767-701-28008

Query Match 8.7%; Score 133; DB 7; Length 464;
Best Local Similarity 58.9%; Pred. No. 4.5e-21;
Matches 248; Conservative 0; Mismatches 170; Indels 3; Gaps 1;

Qy 70 TAGGCTCTCAAAAGCCCGCCCAACATGAGCCGAACTCTTGGGTTCATATGCTTGGCCG 129
Db 43 TCGGCGGCGCCAAAGGCTCCGCGCATAGGCGGAGCTGTGCTCCGCGCACTGGAGG 102
Qy 130 GGTACTTAAACCCGCTCAAGATAGGCTCCGTAGATCTCTTCAAGCTTGGGGGACCTT 189
Db 103 GCTCTGTGACCTCTTCAAGCTCAAGCTCCGCGCTCATCTCTCTGCGGCACTCT 162
Qy 190 GCCAGGTGATATGACACCTTCAATAAAGACCAAGAACTGTCTTACTGCGGAGACCC 249
Db 163 GCCAGGTGATATGATTCCTTCAATCTCAAGCTCAAGCTCAAGTATGATGAGCTGCC 222
Qy 250 GCTACGGAAGGCGGACCTTATTAAGACCGCTTCCGCGGAGGCGCAGACCGTTTG 309

Db 223 GCTACTCAGAGTCCACGCTCTTCGCTCGACGCTGTTCCCGCGCCGAC---ATCT 279
Qy 310 ACGTGTGGCTACTTTGAGCCCACTGGAGATGACGCTCCAGAGCCGTTTCTCTGA 369
Db 280 CCCCCGCGGCTACTCTTACCGACCTCCAGTGTCTCCGCGCGCATGAGGT 339
Qy 370 AGTCAGATCGAGGAGAGATGGATAGGAATGGAATTTGGATGCTGCTGTGT 429
Db 340 TCTGCTCTCCCGGAGGCGGTGAGCAGAGATGCACTGATCGCTACGCTTCCGTGT 399
Qy 430 CGAATGACGAGACGATGCGGTGCGGACGAGAGAGATGATGCTGTGAGAGGGA 489
Db 400 CCAAGACGCGCGCGCGCGCCGACGAGGCGCAGCGCTCATCTAGTGGCGCGCGCA 459
Qy 490 C 490
Db 460 C 460

RESULT 13

US-10-674-540-6
; Sequence 6, Application US/10674540
; Publication No. US20040158891A1
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE.
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; FILE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/10/674,540
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PaeSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 923
; TYPE: DNA
; ORGANISM: Plant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(512)
; NAME/KEY: Intron
; LOCATION: (513)...(843)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (844)...(921)
US-10-674-540-6

Query Match 8.6%; Score 131.8; DB 7; Length 923;
Best Local Similarity 58.2%; Pred. No. 1.3e-20;
Matches 251; Conservative 0; Mismatches 177; Indels 3; Gaps 1;

Qy 666 AAAGCAAGAGAAAGAGAGCAGACGATGATGACGACCCCAAGATGATCAAGGT 725
Db 90 AACAAAGAGAGAGATGAGAGAGAGAGAGAGAGATGAGATCAAGATGATGAGGT 149
Qy 726 TGATGACATATATACATCGAGAGATCCCAATCACTTTCACAAATCAATGTCAGA 785
Db 150 TGGCTTAAGATCTAGCTCAAGTACCCGAAAGTGTCTTTCACGAGACTTAAGTGAAGA 209
Qy 786 AACAACTTGAAGACCAACTCAATCAATGACAAATCAAGAGCAAGACCTAAGC 845
Db 210 GAACAACTTGAAGAGATGAGAGAGATGAGAGAGATGAGATGAGATGAGATGAGC 269
Qy 846 ATAACTTCCGCGGTCAAGGCTAGGCGCGCACTATCACTGTGAGCGCCTTTCAGATA 905

Db 270 ATAACTTACAGGCGCATAGCTTGTGTGATCTTACCTGTTTACCTGATTTGATGTG 329
Qy 906 GTGAGAA---TTCACAGCAGAGATCCAGTACAGGCGCGGTCTTCCGAGTCCCAAA 962
Db 330 GTTGAATAGGTGTGCGCAGTGTGATATTCAGATCTGCAATTTGATTTGATGTCACA 389
Qy 963 GTAGCAACAAATAATTCACAACTCTTGCATCTGATCCCAAACTTAAATGCTCCAT 1022
Db 390 GTTGGAAATAGGATTCATTAAGAGATCAAGAAATTCACAACTTGAATATTTACAT 449
Qy 1023 GTTAAAGATGATCATGATCTGATCTCTGTATCCCTGAAATCATAGGTTTACGTAC 1082
Db 450 GTTAAAGAAAGATGATGATTCATTAATCCCTTACCAAGTCTGTGTTGGATGTAAT 509
Qy 1083 ATAGGATCGA 1093
Db 510 TCAGTATTTGA 520

RESULT 14

US-10-424-599-43547
; Sequence 43547, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 43547
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139321C.1
US-10-424-599-43547

Query Match 8.1%; Score 124.6; DB 7; Length 588;
Best Local Similarity 54.5%; Pred. No. 5.1e-19;
Matches 272; Conservative 0; Mismatches 224; Indels 3; Gaps 1;

Qy 92 AACATGCGCCGAACTCTCTGAGTCCATATGCTTGGCGCGGCTACTAATCCGCTCAACGA 151
Db 33 AAATGAGAGAGACCTCAGTGGCAGAGACATGGAAAGTCTGCTAGATCCTTACGACAT 92
Qy 152 TGAGCTCCGTGAGCTCTCTTACGCTCGGGGACTTTCGCAAGTGCATACGACACTT 211
Db 93 TGATCTTCCGCGTTCATTAATACATATGACAACTTGTCAAGCTCATATGATGTCTT 152
Qy 212 CATTAACGACGAGAACTCTCTGAGTCCATGCTGCGCAGAGCGCTACGAGAAAGGCGACTACT 271
Db 153 CAACTCAGAAAGACATCAAGTATGCTGCGCAGACGCTGATCCCTTAAGAAATTTCTT 212
Qy 272 TCATTAAGACCGCTTCCCGGCGG---CGCAGACCGGTGTGACGTGTGCGTACTTGTGA 328
Db 213 TTCCAAAGTAGTGTGGAAGAAACGAAACCTTTCAAGTACGAGTGAAGATTCCTCTA 272
Qy 329 CGGCATCTGCAAGATCAGCTCCAGAGGCGTTTCTCTGATGCTGAGGTGAGAGGAA 388
Db 273 CGCAACTTCCAAAGCCAGCAGCAGAGAGGCTTCTGCTCAAGTCTTTTCGAAAGACTC 332
Qy 389 GTGGATAGGGAATCGAATTTGATTTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
Db 333 GTGAGAGACCAATCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 392
Qy 449 GGTGGCGGACGAGAGGAGGTGATGTGTGTGAGAGAGGACTTGTGAGGATTAATGATG 508
Db 393 AGCGTTGGGAGAGAGGACATAGTGTGCTTGAAGAGAACTTACAGGCTCGGAAATG 452

Search completed: December 26, 2005, 17:04:09
Job time : 1353.14 Secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: December 26, 2005, 07:53:18 ; Search time 291.822 Seconds
(without alignments)
9362.258 Million cell updates/sec

Title: US-10-674-540A-1
Perfect score: 1537
Sequence: 1 gcacgagccattcccaaac.....ctagtttaaaaaaaaaa 1537

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/1/ina/5.COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/H.COMB.seq:*
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9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	100.0	1537	3	US-09-610-104C-1
2	291.2	18.9	1167	3	US-09-610-104C-15
3	131.8	8.6	923	3	US-09-610-104C-6
4	62.6	4.1	1344	2	US-09-610-104C-18
5	60.6	3.9	7218	2	US-08-232-463-14
6	51	3.3	1141	3	US-09-806-708B-22
7	48.4	3.1	17612	3	US-09-949-016-15061
8	47.2	3.1	32392	3	US-09-662-254B-27
9	46.4	3.0	601	3	US-09-949-016-23927
10	46.4	3.0	67755	3	US-09-949-016-148614
11	45.8	3.0	1663	3	US-08-827-171B-1
12	45.8	3.0	1663	3	US-09-588-995A-88
13	45.8	3.0	1663	3	US-09-596-062-1
14	45.8	3.0	18651	3	US-09-949-002-592
15	45.8	3.0	18682	3	US-09-949-002-786
16	45.8	3.0	640681	3	US-09-790-988-1
17	45.8	3.0	21358	3	US-09-973-278-789
18	45.6	3.0	21676	3	US-09-973-278-792
19	45.6	2.9	40655	3	US-09-949-016-12032
20	45.2	2.9	40655	3	US-09-949-016-15919
21	44.8	2.9	601	3	US-09-949-016-23926
22	44.8	2.9	601	3	US-09-949-016-148613
23	44.8	2.9	100863	3	US-09-949-016-17031
24	44.8	2.9	100863	3	US-09-949-016-17031

C 25	44.6	2.9	55866	3	US-09-949-016-15129	Sequence 15129, A
C 26	44.4	2.9	421118	3	US-09-949-016-16297	Sequence 16297, A
C 27	44.2	2.9	601	3	US-09-949-016-132805	Sequence 132805, A
C 28	44.2	2.9	96878	3	US-09-949-016-12551	Sequence 12551, A
C 29	44.2	2.9	187169	3	US-09-949-016-12776	Sequence 12776, A
C 30	44.2	2.9	191569	3	US-09-949-016-15940	Sequence 15940, A
C 31	44	2.9	700	3	US-09-735-271-1038	Sequence 1038, Ap
C 32	44	2.9	12313	3	US-09-949-016-13248	Sequence 13248, A
C 33	44	2.9	13830	3	US-09-614-981-18	Sequence 8, Appl
C 34	43.8	2.8	17612	3	US-09-949-016-15061	Sequence 15061, A
C 35	43.8	2.8	50000	3	US-09-662-254B-24	Sequence 24, Appl
C 36	43.8	2.8	231129	3	US-09-949-016-16110	Sequence 16110, A
C 37	43.8	2.8	266293	3	US-09-949-016-11934	Sequence 11934, A
C 38	43.6	2.8	20674	3	US-09-641-638-651	Sequence 651, App
C 39	43.6	2.8	20674	3	US-10-170-097-651	Sequence 651, App
C 40	43.6	2.8	51835	3	US-09-949-016-17101	Sequence 17101, A
C 41	43.6	2.8	52032	3	US-09-949-016-11789	Sequence 11789, A
C 42	43.6	2.8	110000	3	US-09-830-902-1	Sequence 1, Appl
C 43	43.4	2.8	1341	3	US-09-830-230A-572	Sequence 572, App
C 44	43.4	2.8	1410	3	US-09-830-230A-571	Sequence 571, App
C 45	43.4	2.8	32099	3	US-09-949-016-16562	Sequence 16562, A

ALIGNMENTS

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RESULT 1
US-09-610-104C-1
; Sequence 1, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE.
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1537
; TYPE: DNA
; ORGANISM: Plant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (48) ... (1390)
US-09-610-104C-1

Query Match 100.0%; Score 1537; DB 3; Length 1537;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCACGAGCCATTCCAAAGCTCTTACACCACTCAAACTATTTCACATGAGCTGCAGAG 60
DB 1 GCACGAGCCATTCCAAAGCTCTTACACCACTCAAACTATTTCACATGAGCTGCAGAG 60
QY 61 CCCAACCTTTAGGCTCTCAAGCCGCGCCCAACATGAGCTCTCGGGTCCATG 120
DB 61 CCCAACCTTTAGGCTCTCAAGCCGCGCCCAACATGAGCTCTCGGGTCCATG 120
QY 121 CTTGGGCGGGGCTCTTAACCCGCTCAACGATGAGCTCCGAGAGCTCTCTTAGGCTGCG 180
DB 121 CTTGGGCGGGGCTCTTAACCCGCTCAACGATGAGCTCCGAGAGCTCTCTTAGGCTGCG 180
QY 181 GGGAGCTCTGCGAGGATGACATGACGACCTTCAATTAAGCAAGAACTGCTGCTACTGCG 240
DB 181 GGGAGCTCTGCGAGGATGACATGACGACCTTCAATTAAGCAAGAACTGCTGCTACTGCG 240
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Db	181	GGGACTTCTGCGAGGTGACATACGACACCTTCATTAAGACGACGAAACTCGCTACTGCG	240
Qy	241	GCAGCAGCCGCTACCGGGAAGCGGACCTACTTCAATAAGACCGCTTCCCGGGGGCGAG	300
Db	241	GCAGCAGCCGCTACCGGGAAGCGGACCTACTTCAATAAGACCGCTTCCCGGGGGCGAG	300
Qy	301	ACCGGTTTGAAGTGGTGGCGTAACTTTGTAACGACCTGGGAAAGTCAAGGCTCCGAGGCGT	360
Db	301	ACCGGTTTGAAGTGGTGGCGTAACTTTGTAACGACCTGGGAAAGTCAAGGCTCCGAGGCGT	360
Qy	361	TTCTCTGAAGTCGAGGTCGAGGGGAGAAGTGGATAGGAATCGAATTGGATTGGGTATG	420
Db	361	TTCTCTGAAGTCGAGGTCGAGGGGAGAAGTGGATAGGAATCGAATTGGATTGGGTATG	420
Qy	421	TCGTGTGTGCAATGACGAGACGAGTCGGGTGGCGGACGAAAGGAGTGAATGTGGTGT	480
Db	421	TCGTGTGTGCAATGACGAGACGAGTCGGGTGGCGGACGAAAGGAGTGAATGTGGTGT	480
Qy	481	GGAGAGGGACTTGTGAGGATTAATGATGGGTGATGTTCTTGATGATCACTTGAAGCTG	540
Db	481	GGAGAGGGACTTGTGAGGATTAATGATGGGTGATGTTCTTGATGATCACTTGAAGCTG	540
Qy	541	CTCATCTCTTGTATGCACTCAACAACTACTCATGTGTAAGAAAGTGGAAATGAGGAAA	600
Db	541	CTCATCTCTTGTATGCACTCAACAACTACTCATGTGTAAGAAAGTGGAAATGAGGAAA	600
Qy	601	AGAAAGCAATTCATTAATCAAGTGGTACGACTGTTTCAATATCACTACTAGGTTCCG	660
Db	601	AGAAAGCAATTCATTAATCAAGTGGTACGACTGTTTCAATATCACTACTAGGTTCCG	660
Qy	661	CGTCCAAAGACAAAGAAAAGGAGCGACGACGATGATGAGAGACCCCAATGATGC	720
Db	661	CGTCCAAAGACAAAGAAAAGGAGCGACGACGATGATGAGAGACCCCAATGATGC	720
Qy	721	AAGTTGATGACATPATACATGAGGAGATCCCAATTCACCTTCACAAACTAATAGT	780
Db	721	AAGTTGATGACATPATACATGAGGAGATCCCAATTCACCTTCACAAACTAATAGT	780
Qy	781	CAAGAACACACTTCAGACCCAACTCAAACTAATAGCAAAAATACAAAGACGAAACC	840
Db	781	CAAGAACACACTTCAGACCCAACTCAAACTAATAGCAAAAATACAAAGACGAAACC	840
Qy	841	TAAAGATTAATTCCTCCCGGTCAAGCTTAAGGCGGACACTATGCTGAGCCCTTCG	900
Db	841	TAAAGATTAATTCCTCCCGGTCAAGCTTAAGGCGGACACTATGCTGAGCCCTTCG	900
Qy	901	AATATGTGAGAAATCAACGACCGAGATCCGAGTACAGGCGGTGCTTGGGGTCCGAA	960
Db	901	AATATGTGAGAAATCAACGACCGAGATCCGAGTACAGGCGGTGCTTGGGGTCCGAA	960
Qy	961	AAGTAGGCAACAAAATTCCAACAACCTTCGACTCGTACCCAACTTAATATGCTCC	1020
Db	961	AAGTAGGCAACAAAATTCCAACAACCTTCGACTCGTACCCAACTTAATATGCTCC	1020
Qy	1021	ATGTAAAGAAATGTCATCGACTGATCCCTGTATCCGTGAATCTCATGCGTTAAGTGA	1080
Db	1021	ATGTAAAGAAATGTCATCGACTGATCCCTGTATCCGTGAATCTCATGCGTTAAGTGA	1080
Qy	1081	ACATAGGAATCGAGCTGAGATCGACTGAGGAAGTCACTTCCTTAAGGAATCGAAAA	1140
Db	1081	ACATAGGAATCGAGCTGAGATCGACTGAGGAAGTCACTTCCTTAAGGAATCGAAAA	1140
Qy	1141	ACCCGAGTATGGGCAATAATTGCAAGCAAAATTCGATGTTGAAGTGGTGGCATGGGG	1200
Db	1141	ACCCGAGTATGGGCAATAATTGCAAGCAAAATTCGATGTTGAAGTGGTGGCATGGGG	1200
Qy	1201	TTAAGGGGAGTTTAAGTTGTAAATAAGAGAAAGTTTGCAATGTTAATAATGATGTG	1260
Db	1201	TTAAGGGGAGTTTAAGTTGTAAATAAGAGAAAGTTTGCAATGTTAATAATGATGTG	1260
Qy	1261	ATTTTCTTAAGAGAAATGTTGGTTCCTCCGAGCTTGGTGGTGTGTGAGAAACAAAGGA	1320
Db	1261	ATTTTCTTAAGAGAAATGTTGGTTCCTCCGAGCTTGGTGGTGTGTGAGAAACAAAGGA	1320

Qy	1321	TGCTTTTGAATAAAGGATGCGAGCGGTTTTGGTCCCTCCGAGGAAGATCCATCCTG	1380
Db	1321	TGCTTTTGAATAAAGGATGCGAGCGGTTTTGGTCCCTCCGAGGAAGATCCATCCTG	1380
Qy	1381	AATTGATGTGATATATTTTCATCATGTGTTTTATTTTTATTAATAATTTTACTAAATTTTCAT	1440
Db	1381	AATTGATGTGATATATTTTCATCATGTGTTTTATTTTTATTAATAATTTTACTAAATTTTCAT	1440
Qy	1441	GACAAATTTATGGAATAAGTTACTTATTTATTTATGTTATTTATTTGAAATGCGTTTTAA	1500
Db	1441	GACAAATTTATGGAATAAGTTACTTATTTATTTATTTATTTGAAATGCGTTTTAA	1500
Qy	1501	GTTACATPAAATTCGCAATTAAGTTTAAAAAAAAAAAAAAA	1537
Db	1501	GTTACATPAAATTCGCAATTAAGTTTAAAAAAAAAAAAAAA	1537

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      RESULT 2
      US-09-610-104C-15
      ; Sequence 15, Application US/09610104C
      ; Patent No. 6774284
      ; GENERAL INFORMATION:
      ; APPLICANT: John E. THOMPSON et al.
      ; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
      ; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
      ; TITLE OF INVENTION: PLANTS
      ; FILE REFERENCE: 10799-10
      ; CURRENT APPLICATION NUMBER: US/09/610,104C
      ; CURRENT FILING DATE: 2000-07-05
      ; PRIOR APPLICATION NUMBER: 09/597,774
      ; PRIOR FILING DATE: 2000-06-09
      ; PRIOR APPLICATION NUMBER: 09/250,280
      ; PRIOR FILING DATE: 1999-02-16
      ; PRIOR APPLICATION NUMBER: 09/105,815
      ; PRIOR FILING DATE: 1998-06-26
      ; NUMBER OF SEQ ID NOS: 21
      ; SOFTWARE: FastSeq for Windows Version 4.0
      ; SEQ ID NO 15
      ; LENGTH: 1167
      ; TYPE: DNA
      ; ORGANISM: Plant
      ; FEATURE:
      ; NAME/KEY: CDS
      ; LOCATION: (1)...(1044)
      US-09-610-104C-15

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Query Match	10.9%	Score 291.2	DB 3	Length 1167
Best Local Similarity	64.3%	Pred. No. 1.1e-67		
Matches 453	Conservative 0	Mismatches 248	Indels 3	Gaps 1
Qy	AGCGACGACGACGATGATGACGACCCCAATGATGCAAGGTGTGAATGACAAATATACACA	743		
Db				
310	AGTGACAGTGAAGATGAAGAAAGGGGTGTAGGTGATGCTCGGGTGGCTCAATCTATACT	399		
Qy	744	TCGGAGATGCCAATTCACCCCTTCACAAACTAAGTGCAGAGACAACTTCAGACCAA	803	
Db				
400	CTTAATACCCCGAATCGAATTTCTCTAAGTGTAGTCTACAGTTCATGTTTAGCCAG	459		
Qy	804	CTCAACACTAATATGACAAATAATACAAAGACGAAACCTTAAGCATTAATTCGCGGTAC	863	
Db				
460	ATCAAGAGCTTCTGTGTAAGTATAGGACGAGAAACGACATTTGTGTACGTGACAT	519		
Qy	864	AGCTTAGCGCGACACTATACAGTCGTGAGCGCCTTCGACATAGTGAGAA--TCTCAG	920	
Db				
520	AGCTTGGGAACTACAGAGAGCTGTCTTGCGCGCCTATGATATAGCTGAGAAAGGTTCCAGT	579		
Qy	921	ACCGAGATCCGAGTACGCGCGGTGTCCTTCGGGTGCCCAAAAGTAGGCAAAATAATTC	980	
Db				
580	GATGATGTTCGGGTCACTGCTATAGTCTTTGGTTGTCCACAGTAGGAAACAAAGAGTTC	639		
Qy	981	CACCAACTCTTGACTCGTACCACCACTAAATGTCTTCATGTAGGAATGTCAATGCAC	1040	

Db	640	AGAGACGAAGTAATAGTGCACAAGAACTTAAAGATCTCCATGTAAGAAACAAGATTAT	699
Qy	1041	CTGATCCCTCTGTATCCCGTGAATCATAGGGTTACGTAAACAATAGAAATTCGAGCTGAG	1100
Db	700	CTCTTAACTCGATACCTCAAGGGGGACTTTTATGGGTATGTGACAATAGAAATTAACCTTTG	759
Qy	1101	ATCGACTCGAGGAGTCGACCTTTCTTAAAGGACGTGAAAAACCCGATATGGGCATAT	1160
Db	760	ATCGATACAAAGAGTCACCGTTCCCTCAACCGATTCAAGGAATCCAGGGGATTTGGCATAT	819
Qy	1161	TTGCAAGCAATATTTCGATGTTGTAAAGTGGTGCATAGGGGTTAAGGGGAGTTTAAGTT	1220
Db	820	CTTACGGGATCTTACATGTTTACGTGGAATGGAATGGAAGAAAGAAAGATTTAAC	879
Qy	1221	GTAAATTAAGAAAGTGTGCATTGGTTAAATTAATCATGTGATTTTCTTAAGAAAGATGT	1280
Db	880	ATGCTTAAGAAAGATATGCATTAGTAACAAGTCAATCGAGTCTTGAAGCTGAGTGT	939
Qy	1281	TTGGTTCTCCAGCTTTGTGGGTTGTGCAGAACAAAGGATGGTTTTGAATTAAGATGGT	1340
Db	940	TTGGTGCAAGATCTTTGGTGGGTAAAGAAACAAGGACTATCAAGAACGAATGTGT	999
Qy	1341	GAGTGGGTTTGGCTCTCTCTGAGGAAAGATCTTACTCTCGAATTT	1384
Db	1000	GAAATGGTCTTCTCCGCTTGAAGAAAGAACTGTACTGAATTT	1043

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US-09-610-104C-6
; Sequence 6, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610.104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 923
; TYPE: DNA
; ORGANISM: Plant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(512)
; NAME/KEY: Intron
; LOCATION: (513)...(843)
; NAME/KEY: CDS
; LOCATION: (844)...(921)
US-09-610-104C-6

Query Match      8.6%; Score 131.8; DB 3; Length 923;
Beet Local Similarity 58.2%; Pred. No. 5e-25;
Matches 251; Conservative 0; Mismatches 177; Indels 3; Gaps 1;

QY      AAAGCAAGGAAAAAGGAAGCGACGACGATGATGACGACCCCAAGTGTGCAAGT 725
      |||||
DB      90  AACCAACGAAGCGATGAGGATGAGACGAGGAGGAGATCAAGTAAATGATGGG 149
      |||||

QY      TGGATGACAAATATACATCGGAGATCCCAATACACCTTGACAAAATTAAGTGCAGA 785
      |||||
DB      150 TGGCTTAAGATTAGTGTCTCAAGTAACCCGAAGTGTCTTTTCACGAGACTTAAGTGAAGA 209
      |||||

QY      ACACAACTTCAGACCAAACTCAACAACTAATGACAAAATACAAAGACGAAACCTTAAGC 845
      |||||

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Db 210 GACACACTTCCAGCAAGATGTGAAAGTTAAGAAATGAGTATTAAGAATGAGAAATTTGAGC 269
OY 846 ATAAACATTGCGCGGTCCACAGCCTTAGGCGCGACATATCAGTCGTGAGCGCCTTGACATA 905
Db 270 ATAACCTTTTACAGGGCACAATGCTTGAGTGTGCTAGCTAGCTGTGTTTAAAGCTTCAATTGATGTG 329
OY 906 GTGAGAGA---TTCACGACCCGAAATGCCATATGCCATACGCGCGGTCTTGCGGATGCCAATA 962
Db 330 GTTGAATAATGATGTGCCAGTTGATATTTCAATATCTGCAATATGATATTTGGTAGTCACAA 389
OY 963 GTAGGCAACAATAATTCACAACAATCTTTCAGCTGTACCCCAAACTTAATATGCTCCAT 1022
Db 390 GTTGGGAATAAGCATTTCAATGAAGAATCAAGAAATTTCTCAACTTGAATATCTTACAT 449
OY 1023 GTAAAGAAATGATCAGACCTGATCCCTGTATCCCGTGAATCTATGCGTTACGTGAAC 1082
Db 450 GTTAAGAACCAAGATGATCTATTAACCTTATCCCAAGTGTCTGTGTTGGGATGTGAAT 509
OY 1083 ATAGGAATCGA 1093
Db 510 TCAGGTATTTGA 520

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US-09-610-104C-18
RESULT 4
; Sequence 18, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1344
; TYPE: DNA
; ORGANISM: Plant
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)...(1344)
US-09-610-104C-18

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	Query Match	Similarity	Score	DB	Length
	Best Local	51.2%	Pred. No. 2e-06		
	Matches	146	Conservative	0	Mismatches 139; Indels 0; Gaps 0
Qy	1070	GGGTTACGTGAACA	TAGGAATCGACTGGAGATCGACTCGAGGAAGTCGACCTTCTTAA	1123	
Db	978	GTGTTATATGACACG	ATGGGGGAGAGCTGGCCGTTGGATCATCAGAACTCGCGTTTCTTAA	1033	
Qy	1130	GGACTTCGAAAAA	CCCCAGTGAATTGGCATTAATTGGCAACGAAATATTCGATGTTTGAAGTG	1189	
Db	1038	ACCTTCGCTGATGTTT	CTACTGCTCATTAATCTGGAAGCTAATGCTCAATTACTTACTTGACGG	1097	
Qy	1190	TTGGCATGGGTTAAG	GGGGAGTTTAAAGTTGTAATTAAGAAAGTGTTCATTTGGTTTA	1248	
Db	1098	GTATCATGAAAAA	GGAAGAGATATTGTGCTGTCAAGTGGAGAGACCATGCGTATGAA	1157	
Qy	1250	TAAATCATATGATTTT	CTTAAGGAAGAAATGTTTGCTTCCACAGTCTGTTGGTTTGCA	1308	
Db	1158	CAAAAGCGTCGACAT	TTTGAAGAAGCATTTACAAATTCACCGTTTGGCTCAAGACGC	1217	


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Query Match          3.0%; Score 46.2; DB 3; Length 67755;
Best Local Similarity 56.1%; Pred. No. 0.35;
Matches 87; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY      1382  ATTGATGTAATAATTTTCATCGTTTAAATTTTATAAATTTTACTAAATTTACATG 1441
DB      40903  ATATTATATATTTTATAATAATAATAATAATAATAATATATATATATATATATATATAT 4096

QY      1442  ACAATTTATGCGACTAGTACTTATATATGTTATATATTTGAAATGCTTTAAG 1501
DB      40963  ATATATATATATATATATATTTAATTAATTAATATATATATATATATATATATATATATATA 4102

QY      1502  TTACATMAAATTGCAATTGCTTTAAAAAATAA 1536
DB      41023  TTATATMAAATAATAATAATATATATATATAATA 41057

RESULT 12
US-08-827-171B-1
; Sequence 1, Application US/08827171B
; Patent No. 6254869
;
GENERAL INFORMATION:
APPLICANT: CAROLYN PETERSEN
APPLICANT: JIN-XING HUANG
TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,
PEPTIDES, DNA AND RNAs FOR PROPHYLAXIS,
TITLE OF INVENTION: TREATMENT, DIAGNOSIS AND
DETECTION OF
TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIK A
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: California
COUNTRY: United States of America
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
COMPUTER: PC
OPERATING SYSTEM: WINDOWS
SOFTWARE: Wordperfect 6.0a WINDOWS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,171B
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,233
FILING DATE: March 27, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hana VERNY
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: (HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-1677
TELEFAX: (415) 324-1678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1663 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
ORIGINAL SOURCE:
ORGANISM: Cryptosporidium parvum
US-08-827-171B-1

Query Match          3.0%; Score 45.8; DB 3; Length 1663;
Best Local Similarity 59.7%; Pred. No. 0.072;
Matches 77; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY      1382  ATTGATGTAATAATTTTCATCATGTTTAAATTTTATAAATTTTACTAAATTTACATG 1441

```

Db 131 ATTGCATGCAATTAATGCGCATGTCATGTTTTCAGAAATTAATAATGACATG 190
Qy 1442 ACAATTATGGGACTAGTACTATTTATATTTTATATTTGAAATGTTTAAAG 1501
Db 191 ACAAGATATTCAAAAAATTGATGATTAATGTTGAAGTTAAATGAAAAAGTAAT 250
Qy 1502 TTACATAAA 1510
Db 251 TAACTAAAA 259

RESULT 13

US-09-588-995A-88
; Sequence 88, Application US/09588995A
; Patent No. 6514697
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: BARNES, DEBRA A.
; APPLICANT: NELSON, RICHARD C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
; TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
; TITLE OF INVENTION: INFECTIONS
; FILE REFERENCE: 480.19-5
; CURRENT APPLICATION NUMBER: US/09/588,995A
; CURRENT FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 08/827,171
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/928,361
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 08/700,651
; PRIOR FILING DATE: 1996-08-14
; PRIOR APPLICATION NUMBER: 08/415,751
; PRIOR FILING DATE: 1995-04-03
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 88
; LENGTH: 1663
; TYPE: DNA
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-88

Query Match 3.0%; Score 45.8; DB 3; Length 1663;
Best Local Similarity 59.7%; Pred. No. 0.072; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 1382 ATTGATGTAATTAATTCATGTTTATTTTATTAATAATTTTAAATTTACATG 1441
Db 131 ATTGCATGCAATTAATGCGCATGTCATGTTTTCAGAAATTAATAATGACATG 190
Qy 1442 ACAATTATGGGACTAGTACTATTTATATTTTATATTTGAAATGTTTAAAG 1501
Db 191 ACAAGATATTCAAAAAATTGATGATTAATGTTGAAGTTAAATGAAAAAGTAAT 250
Qy 1502 TTACATAAA 1510
Db 251 TAACTAAAA 259

RESULT 14

US-09-598-062-1
; Sequence 1, Application US/09598062
; Patent No. 6739044
; GENERAL INFORMATION:
; APPLICANT: CAROLYN PETERSEN
; APPLICANT: JIN-XING HUANG
; TITLE OF INVENTION: CRYPTOPAIN VACCINES, ANTIBODIES, PROTEINS,
; PEPTIDES, DNA AND RNAs FOR PROPHYLAXIS,
; TREATMENT, DIAGNOSIS AND
; DETECTION OF
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIK A

STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: California
COUNTRY: United States of America
ZIP: 94306-1840
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: WINDOWS
; SOFTWARE: Wordperfect 6.0a WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/598,062
FILING DATE: 20-Jun-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/827,171
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/014,233
FILING DATE: March 27, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hana Vervy

REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: (HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-1677
TELEFAX: (415) 324-1678

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1663 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA

ORIGINAL SOURCE:
ORGANISM: Cryptosporidium parvum
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-598-062-1

Query Match 3.0%; Score 45.8; DB 3; Length 1663;
Best Local Similarity 59.7%; Pred. No. 0.072; Indels 0; Gaps 0;
Matches 77; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 1382 ATTGATGTAATTAATTCATGTTTATTTTATTAATAATTTTAAATTTACATG 1441
Db 131 ATTGCATGCAATTAATGCGCATGTCATGTTTTCAGAAATTAATAATGACATG 190
Qy 1442 ACAATTATGGGACTAGTACTATTTATATTTTATATTTGAAATGTTTAAAG 1501
Db 191 ACAAGATATTCAAAAAATTGATGATTAATGTTGAAGTTAAATGAAAAAGTAAT 250
Qy 1502 TTACATAAA 1510
Db 251 TAACTAAAA 259

RESULT 15

US-09-949-002-592/c
; Sequence 592, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH INFLAMMATORY POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 592
; LENGTH: 18651

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 02:34:17 ; Search time 980.564 Seconds
(without alignments)
10446.670 Million cell updates/sec

Title: US-10-674-540A-1

Perfect score: 1537
Sequence: 1 gccgcggccctcccaaac.....ttagtttaaaaaaaaaa 1537

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1535.4	99.9	1537	3	AAAS3880 Senescenc
2	1535.4	99.9	1537	6	AAAS20751 CDNA enco
3	1531.4	22.9	1239	6	ABZ14677 Arabidops
4	1531.4	22.9	1239	13	ADU20461 A. thalia
5	1531.4	22.9	1239	13	ADU20461 A. thalia
6	1531.4	22.9	1239	13	ADU20461 A. thalia
7	291.2	18.9	1167	6	AAAS3885 Arabidops
8	291.2	18.9	1167	6	AAAS20756 Arabidops
9	169.4	11.0	1077	11	ACL26423 Rice abio
10	165.6	10.8	1077	11	ACL26423 Rice abio
11	165.6	10.8	1077	11	ACL26423 Rice abio
12	151	9.8	1384	13	ADK60584 Plant ful
13	131.8	8.6	923	3	AAAS3884 Senescenc
14	131.8	8.6	923	3	AAAS20753 Partial g
15	111.6	7.3	1353	8	ADA69968 Rice gene
16	109.6	7.1	594	12	ADJ44250 Plant CDN
17	105.6	6.9	2043	13	ADK61747 Plant ful
18	104.6	6.8	1197	8	ADA69856 Rice gene
19	101.4	6.6	1396	3	AAAC41939 Arabidops

20	101.4	6.6	1398	3	AAAC41529 Arabidops
21	101.4	6.6	1400	3	AAAC40763 Arabidops
22	101.4	6.6	1417	13	ADT15180 Plant CDN
23	98.4	6.4	1589	13	ADT18913 Plant CDN
24	93	6.1	1576	13	ADK48486 Plant ful
25	92	6.0	1522	13	ADK32777 Plant ful
26	92	6.0	2008	13	ADK34216 Plant ful
27	91	5.9	1591	13	ADK3756 Plant ful
28	90.4	5.9	1878	13	ADK48110 Plant ful
29	90.4	5.9	1927	13	ADK32745 Plant ful
30	86.4	5.6	1164	8	ADA69718 Rice gene
31	85.4	5.6	1536	13	ADK28155 Plant ful
32	85.4	5.6	1627	13	ADK28082 Plant ful
33	81.2	5.3	6777	11	ACL312126 Rice abio
34	77.4	5.0	240	10	ADK31758 Rice abio
35	77	5.0	1518	13	ADK10037 Plant ful
36	76.8	5.0	1641	13	ADK28068 Plant ful
37	71.6	4.7	1507	13	ADK50603 Plant ful
38	65.4	4.3	229	12	ADJ10834 Recombina
39	65.2	4.2	779	10	ADJ18245 Barley ge
40	62.6	4.1	636	13	ADK2858 Plant ful
41	62.6	4.1	1344	6	ABZ13508 Arabidops
42	62.6	4.1	1344	6	AAAS20757 CDNA enco
43	62.6	4.1	1344	8	ADA67881 Arabidops
44	62.6	4.1	1758	3	AAAC48392 Arabidops
45	62.6	4.1	1760	3	AAAC39568 Arabidops

ALIGNMENTS

RESULT 1	AAAS3880	standard; CDNA; 1537 BP.
ID	AAAS3880	
AC	AAAS3880;	
DT	03-JAN-2001	(first entry)
DE	Senescence-induced lipase coding sequence.	
XX	Senescence-induced lipase; senescence; lipase; antisense; regulation;	
XX	modulation; resistance; stress; crop protection; ethylene; ds.	
OS	Dianthus caryophyllus.	
XX		
XX	Key	Location/Qualifiers
XX	CDS	47..1391
XX		/*tag= a
XX		/product= "Senescence-induced lipase"
XX		
XX	MO200049164-A1.	
XX	24-AUG-2000.	
XX		
XX	14-FEB-2000; 2000MO-US003494.	
XX		
XX	16-FEB-1999; 99US-00250280.	
XX		
XX	(SENESC-) SENESCO INC.	
XX		
XX	Thompson JB, Wang T, Hudak K, Hong Y;	
XX		
XX	WPI; 2000-549277/50.	
XX	P-PSDB; AAY97298.	
XX		
XX	DNA encoding carnation senescence-induced lipase, useful for regulating	
XX	the expression of senescence in plants to delay its onset and improve	
XX	plant resistance to environmental stress, thus extending shelf-life or	
XX	growth period.	
XX	Claim 1; Page 70; 89pp; English.	

CC insertion of the senescence-induced lipase coding sequence in an
 CC antisense direction in a plant genome can be used to regulate the
 CC expression of senescence in those plants. Alteration of expression of the
 CC senescence-induced lipase gene in plants results in delayed onset of
 CC senescence and improved resistance to environmental stress, thus
 CC extending the plant shelf-life and/or growth period. The genetically
 CC altered plant is useful for producing a new variety or line of plants
 CC where the alteration is stably transmitted from generation to generation.
 CC This method of regulation is advantageous over prior senescence
 CC modulating technologies since prior methods were only applicable to a
 CC limited range of plants, e.g. to plants that are ethylene-sensitive. The
 CC antisense regulation method is applicable to all types of plants,
 CC regardless of ethylene sensitivity

XX Sequence 1537 BP; 448 A; 329 C; 381 G; 379 T; 0 U; 0 Other;

Query Match 99.9%; Score 1535.4; DB 3; Length 1537;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1536; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GCACAGCCATTCCAAAACCTCTTACACCACTCAAAATATTCACATGCGTGCAGAG 60
DB 1 GCACAGCCATTCCAAAACCTCTTACACCACTCAAAATATTCACATGCGTGCAGAG 60
QY 61 CCCAACCTTAGGCTCTCAAAAGCCGCGCCCAACATGCGCCGAATCCTCGGATCCATG 120
DB 61 CCCAACCTTAGGCTCTCAAAAGCCGCGCCCAACATGCGCCGAATCCTCGGATCCATG 120
QY 121 CTTGGGCGGCGCTACTAAACCCGCTCAACGATGAGCTCCGAGCTCCTCTCAAGCTGCG 180
DB 121 CTTGGGCGGCGCTACTAAACCCGCTCAACGATGAGCTCCGAGCTCCTCTCAAGCTGCG 180
QY 181 GGGACTTCTGCAGGTGATCAATGACACCTTATTAAGACAGACGCTGCTACTAGTGG 240
DB 181 GGGACTTCTGCAGGTGATCAATGACACCTTATTAAGACAGACGCTGCTACTAGTGG 240
QY 241 GCACAGCCGCTTACGGAAGGCGGACCTACTTCAATAGACCGCTTCCCGGGGCGGAG 300
DB 241 GCACAGCCGCTTACGGAAGGCGGACCTACTTCAATAGACCGCTTCCCGGGGCGGAG 300
QY 301 ACCGGTTGACGTGCGTGCCTTGTATGCCCATGCGAAGGTCAAGCTCCAGAGGCGT 360
DB 301 ACCGGTTGACGTGCGTGCCTTGTATGCCCATGCGAAGGTCAAGCTCCAGAGGCGT 360
QY 361 TTCTGCTAAGTCCGAGGTGCGAGGGAAGTGGGAATCGAATTGGATGGGTATG 420
DB 361 TTCTGCTAAGTCCGAGGTGCGAGGGAAGTGGGAATCGAATTGGATGGGTATG 420
QY 421 TCGTGTGTCGATGACGACGAGTCCGAGTGGCGGAGCGAAGGAGGTGTATGTGTGT 480
DB 421 TCGTGTGTCGATGACGAGAGTCCGAGTGGCGGAGCGAAGGAGGTGTATGTGTGT 480
QY 481 GGAGAGGACCTTGTAGGATTAATGAGTGGTGTATGTTCTTGGTCTCAACTTGAAGTCTG 540
DB 481 GGAGAGGACCTTGTAGGATTAATGAGTGGTGTATGTTCTTGGTCTCAACTTGAAGTCTG 540
QY 541 CTCACTCTTTTGTATGCGACTCAACAACTACTCATGTGTAAGGATGGAATGAGGAAA 600
DB 541 CTCACTCTTTTGTATGCGACTCAACAACTACTCATGTGTAAGGATGGAATGAGGAAA 600
QY 601 AGAAGAGCATTCATTAATCAAGTTGTGTAAGTCTTCAATATCAACCTACTAGGTTCCG 660
DB 601 AGAAGAGCATTCATTAATCAAGTTGTGTAAGTCTTCAATATCAACCTACTAGGTTCCG 660
QY 661 CGTCCAAAGCAAAAGAAAGAGGAGCGACGACGATGATGACGACCCCAAGTATGATGC 720
DB 661 CGTCCAAAGCAAAAGAAAGAGGAGCGACGACGATGATGACGACCCCAAGTATGATGC 720
QY 721 AAGGTGATGATCAATATATACATGAGAGATCCCAATCACCCTTCAACAAATCTAAGTG 780
DB 721 AAGGTGATGATCAATATATACATGAGAGATCCCAATCACCCTTCAACAAATCTAAGTG 780
QY 781 CAAAGAACAACTTGAAGCAAACTCAAAACAATATGACAAATATCAAAAGACGAAACCC 840

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DB 781 CAAAGAACAACTTGAAGCAAACTCAAAACAATATGACAAATATCAAAAGACGAAACCC 840
QY 841 TTAAGCATTAATTCGCGCGTCAACGCTTACGCGGACATATCATGCTGATGAGCCCTTTCG 900
DB 841 TTAAGCATTAATTCGCGCGTCAACGCTTACGCGGACATATCATGCTGATGAGCCCTTTCG 900
QY 901 ACATATGAGAAATCTGACGACCGAGATCCCATGTCAGCGCCGTGTCTTGGGATGCCCA 960
DB 901 ACATATGAGAAATCTGACGACCGAGATCCCATGTCAGCGCCGTGTCTTGGGATGCCCA 960
QY 961 AAGTATGCAACAAAATTTTCAACATCTTCACTGCTGATCCCAAACTTAATGTCCTCC 1020
DB 961 AAGTATGCAACAAAATTTTCAACATCTTCACTGCTGATCCCAAACTTAATGTCCTCC 1020
QY 1021 ATCTAAGAAATGTCATGACCTGATCCCTCTGTATCCCGTAAACTATGAGTATCGTGA 1080
DB 1021 ATCTAAGAAATGTCATGACCTGATCCCTCTGTATCCCGTAAACTATGAGTATCGTGA 1080
QY 1081 ACATGAGAAATCGAGCTGAGATCGACTCGAAGAGTCACTTCTTAAAGACTCGAAAA 1140
DB 1081 ACATGAGAAATCGAGCTGAGATCGACTCGAAGAGTCACTTCTTAAAGACTCGAAAA 1140
QY 1141 ACCGAGTATGTCATTAATTTTGCACGATATTTGCATGTTGTATGAGTGTGATGAGG 1200
DB 1141 ACCGAGTATGTCATTAATTTTGCACGATATTTGCACGATATTTGCATGTTGTATGAGG 1200
QY 1201 TTAAGGGGAGTTTAAAGTTGTAATTAAGAAAGTGTGATGCTTGAATTAATGATCATGTG 1260
DB 1201 TTAAGGGGAGTTTAAAGTTGTAATTAAGAAAGTGTGATGCTTGAATTAATGATCATGTG 1260
QY 1261 ATTTCTTAAAGAAATGTTTGTCTTCCAGCTTGTGAGTGTGTCAGAACAAAGGGA 1320
DB 1261 ATTTCTTAAAGAAATGTTTGTCTTCCAGCTTGTGAGTGTGTCAGAACAAAGGGA 1320
QY 1321 TGTGTTGTAATTAAGATGATGAGTGTGCTTCTCTCTGAGAGAAATCTCTCTCTG 1380
DB 1321 TGTGTTGTAATTAAGATGATGAGTGTGCTTCTCTCTGAGAGAAATCTCTCTCTG 1380
QY 1381 AATTGATGATTAATTTTCAATGTTTATATTTTATTAATTTTACTTAATTTTACAT 1440
DB 1381 AATTGATGATTAATTTTCAATGTTTATATTTTATTAATTTTACTTAATTTTACAT 1440
QY 1441 GACAAATTAAGGAGCTAAGTACTTATTAATGTTTATTAATTTTAAATGTTTAA 1500
DB 1441 GACAAATTAAGGAGCTAAGTACTTATTAATGTTTATTAATTTTAAATGTTTAA 1500
QY 1501 GTTACATTAATTTGCAATTTGTTTAAAAAAA 1537
DB 1501 GTTACATTAATTTGCAATTTGTTTAAAAAAA 1537

RESULT 2
AAS20751
ID AAS20751 standard; cDNA; 1537 BP.
XX
XX AAS20751;
XX
XX 09-APR-2002 (first entry)
XX
XX cDNA encoding carnation senescence-induced lipase.
XX
XX Plant; senescence-induced lipase; regulation of senescence;
XX environmental stress; carnation; gene; 88.
XX
XX Dianthus caryophyllus.
XX
XX Key Location/Qualifiers
XX CDS 48..1391
XX FT /*tag= "a
XX FT /product= "Senescence-induced lipase"
XX FT /transl_except= (pos:255..257, aa:Glu)
XX

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PN WO200198510-A2.
XX 27-DEC-2001.
XX 19-JUN-2001; 2001WO-US019385.
XX 19-JUN-2000; 2000US-00597774.
XX 05-JUL-2000; 2000US-00610104.
XX (SENSE-) SENSECO TECHNOLOGIES INC.
XX Thompson JE, Wang T, Hudak K, Hong Y;
XX WPI: 2002-1130793/17.
XX P-PSDB; AAU11997.
XX
XX New carnation and Arabidopsis genes encoding a senescence-induced lipase,
XX useful for controlling (onset of) senescence in plants, regulating
XX expression of senescence in plants, or modifying senescence in transgenic
XX plants.
XX
XX Claim 2, Fig 7, 106pp; English.
XX
XX The present invention relates to the isolation of polynucleotide
XX sequences encoding plant (carnation and Arabidopsis) senescence-induced
XX lipases. Regulation of expression of senescence in plants is obtained by
XX integration of a gene or gene fragment encoding senescence-induced lipase
XX into the plant genome. The isolated polynucleotide sequences are useful
XX for controlling senescence or the onset of senescence in plants caused by
XX either internal or external factors (e.g. environmental stress), or
XX regulating expression of senescence in plants. The DNAs are also useful
XX for modifying senescence in transgenic plants. The present sequence
XX encodes for carnation senescence-induced lipase
XX
XX Sequence 1537 BP; 448 A; 329 C; 381 G; 379 T; 0 U; 0 Other;
SQ
Query Match 99.9%; Score 1535.4; DB 6; Length 1537;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1536; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCACGAGCCATTCGAAACCTCTTACACCACTCAAACTATTCGAAACATGCTGCAGAG 60
DB 1 GCACGAGCCATTCGAAACCTCTTACACCACTCAAACTATTCGAAACATGCTGCAGAG 60
QY 61 CCCAACCTTTAGGCTCTCAAAAGCCGGCCCAACATGCGCCGAACTCTCGGCTCAATG 120
DB 61 CCCAACCTTTAGGCTCTCAAAAGCCGGCCCAACATGCGCCGAACTCTCGGCTCAATG 120
QY 121 CTTGGGCGGGCTTAAACCGGCTCAACGATGAGCTCGGAGCTCTCTAGGCTGCG 180
DB 121 CTTGGGCGGGCTTAAACCGGCTCAACGATGAGCTCGGAGCTCTCTAGGCTGCG 180
QY 181 GGAAGCTTCTGCAGAGTGAATGACACCTTCAATTAAGACGACGATCTGCTCACTGCG 240
DB 181 GGAAGCTTCTGCAGAGTGAATGACACCTTCAATTAAGACGACGATCTGCTCACTGCG 240
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DB 241 GCACGAGCCGCTTACGAGAGCGGACCTTATTCATTAAGACGCTTCCCGGGGGGCGCAG 300
QY 301 ACCGGTTTGAAGTGTGCGCTTATTCATTAAGACGCTTCCCGGGGGGCGCAG 360
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QY 361 TTCTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
DB 361 TTCTGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 420
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DB 481 GGAAGGGAATTTGAGGATTAATGAGTGGGTTGATGTTCTTGTGCTCAACTGAGTGTG 540
QY 541 CTGATCTTTGTTAGCAGATCTCAACAACTCACTCATGTTGAAAAGGTGAAAATGAGAAA 600
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QY 781 CAAGACACAACCTTCAAGCCAACTCAAACTCAATGACAAATATCAAAAGACGAAACC 840
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QY 841 TAAACATTAATTCGCGGTCACAGCCTAGCGGACATATCAGTGTGAGCGCTTGC 900
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QY 901 ACATATGAGAAATCTACGACGACGAGATCCGATCAGCGCGGTCTTGGGTCGCA 960
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QY 1081 ACATAGAAATGACCTGAGATGACGATCGAGAAAGTGCACCTTCTTAAAGATCGA 1140
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QY 1141 ACCGAGTGAATGGCATTAATTTGCAAGCAATATGCAATGTTGAAGTGGATGGG 1200
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QY 1201 TTAAGGGGAGTTTAAAGTGTGTAATTAAGAAAGTGTGCAATGATGATG 1260
DB 1201 TTAAGGGGAGTTTAAAGTGTGTAATTAAGAAAGTGTGCAATGATGATG 1260
QY 1261 ATTTCTTAAAGAAATGTTGTTCTCCAGCTGTGTTGTTGTTGTTGTTGTTGTTGTTG 1320
DB 1261 ATTTCTTAAAGAAATGTTGTTCTCCAGCTGTGTTGTTGTTGTTGTTGTTGTTGTTG 1320
QY 1321 TGGTTTGAATTAAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1380
DB 1321 TGGTTTGAATTAAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1380
QY 1381 AATTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
DB 1381 AATTGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
QY 1441 GACAATTAATGAGCTAAGTTACTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
DB 1441 GACAATTAATGAGCTAAGTTACTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
QY 1501 GTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1537
DB 1501 GTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1537

RESULT 3

AB214677
ID AB214677 standard; DNA; 1239 BP.
XX
AC AB214677;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2482.
XX
KM Arabidopsis thaliana; plant; gene; stress; transgenic; de.
XX
OS Arabidopsis thaliana.
XX
PN W0200216655-A2.
XX
PD 28-FEB-2002.
XX
PE 24-AUG-2001; 2001WO-US026685.
XX
PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0254647P.
PR 22-JUN-2001; 2001US-0300111P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Harper JF, Krepe J, Wang X, Zhu T;
XX
DR WPI; 2002-304127/34.
XX
PT Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
XX Claim 144; SEQ ID NO 2482; 577bp + Sequence Listing; English.
XX
PS The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stresses. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1239 BP; 346 A; 249 C; 323 G; 321 T; 0 U; 0 Other;
Query Match 22.9%; Score 351.4; DB 6; Length 1239;
Best Local Similarity 57.9%; Pred. No. 3.7e-73;
Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;
QY 89 CCCAATGAGGCGCCGAACTCTCGGGTCCAAATGCTTGGCGCGGACTTGTCCAGTGAATAGACAC 148
DB 15 CACATCATGGGAAGAACTCTTAGGCTCAAAAGAAATTTGGAGACATATCTTAGACCCATTGA 74
QY 149 CGATGAGCTCCGTGAGCTCTCTTAAGCTGCGGGGACTTGTCCAGTGAATAGACAC 208
DB 75 CCAATCATTTAGGGAAGCTCATCTTACGTTGTGGGCACTTTGTCAAGCACTAGATGAC 134
QY 209 CTTTCAATTAAGCAAGAACTGCTCTACTGCGGCAAGCGGCTTACGGGAAGCGGACT 268
DB 135 CTTGCTCAACGACCAAACTCCAAAGTACTGTGAGCCAGCGCTACGGCAATCTTCTTT 194
QY 269 ACTTCATAGAACCGGCTTCCGGGGGGGAGACCGGTTTGAAGGTTGAGGCTTACTTGA 328
DB 195 CTTGCAAG--GTCATGCTCGAAACGCTTCCAGTACAGAGTTGTAACCTTCTCTA 251
QY 329 GCGCACTCGAAGTCAAGGTCAGAGTCCAGAGCGGTTTGTGCTGAAGTCAAGGTCAGAGGAA 388
DB 252 GCGCAAGCTGCTGTTTCTCTCCCGAAGGTTTGTCTTCCATCATCAATCAAGAGATTC 311

QY 389 GTGGATAGGAAATCGAATTGGAATTGGGTAATGTCGTGTGCAATGACAGACGACTCG 448
DB 312 TTGGGACCGTGAAGCTTAACGTTTGGCTACATGCTGTCAAGCTGATGAACGGTCTAA 371
QY 449 GGTGGCGGAGCAAGGAGGTGTAATGTGTGTGAGAGGGAATTTGTGGATTAATGAGTG 508
DB 372 GGTCTTGAAGCGCGGTGAAGATCTAATATAGCTTTGAGAGGAACGAGCGAACTATGAGTG 431
QY 509 GGTGATGTTCTTGTGCTCAACTGAGTGTGCTCATCTTGTGTAAGCACTCAACAAAC 568
DB 432 GGTCAATGTTTGTGCTTACGAGCACTTACGCTGACCCCTTGTGCAAGCCGAGCA 491
QY 569 TACTCATGTTGAAAAGGTGAAAATGAGAAAAGAGAGCATTCATTAATCAAGTTGTA 628
DB 492 GGAATGTTCTGGTGTGTATGTA-----GTA 520
QY 629 CGACTGTTTCAATATCAACCTACTAGGTTCCGCTCCAAAGACAAAGAAAAGAGACGA 688
DB 521 CGACTTTT-----GATAGTGA 536
QY 689 CGACGAGATGATGACGACCCCAAGATGATGCAAGTTGATGACAAATATACATGCGA 748
DB 537 CAGTGAAGATGAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596
QY 749 GGAATCCCAATCAACCTTCAAAATTAAGTGCAGAAACAACCTTGCAGACCAACTCAA 808
DB 597 TCACCCGGAATCGAATTCATGCTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 656
QY 809 ACAATTAATGAACAAATTAACAAAGCAAGCAACCTTAAGATTAATCTCCGCTGACACCT 868
DB 657 GGAAGCTTCTGTGAAGTAAAGAGCAAGAAACCGAGATTTGTGTGACTGGAACATAGCTT 716
QY 869 AGGCGGACACTATCACTGTGAGCGGCTTCAATGTGAGAA---TCTCAGACCGA 925
DB 717 GGGAGCTACAGAGGCTGTCTGCGGCTATGATATGATGAGTGAACGGTTCACATGTA 776
QY 926 GATCCAGTCAACGCGCGGTGCTTGGGTCGCCAAAGATAGGCAACAAATTCACACA 985
DB 777 TGTTCGGCTCACTGTATAGCTTTGTTGTGTCACAGTGAAGAAACAGAGGTTCAAGGA 836
QY 986 ACTCTGCACTGTACCCAACTTAATGTCTTCATGTAAGAAATGTCATGCACTGAT 1045
DB 837 CGAAGTATGATGATCAAGAACTTAAGATCTTCATGTAAGAAACAGATGATCTCTT 896
QY 1046 CCTCTGTATCCGTGAACCTCATGAGTACGTGAACATGAGATTCAGCTGAGATCGA 1105
DB 897 AACTCGATACCCAGGGGACTTTTAAAGGTATGAGATGAGAACTTTGTGATCGA 956
QY 1106 CTGAGGAAGTGCACCTTCTTAAGACTCGAAACCCGAGTGAATGGCATTAATTTGCA 1165
DB 957 TACAAAGATGACACCTTCTTACAGATTCAGAGAAATCCAGGGATTTGCAATCTTCA 1016
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DB 1017 GGCATGTTACATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1076
QY 1226 TAAAGAAATGTTGATTTGTTAATAGTCAATGATTTTCTTAAGAAAGAAATTTTGGT 1285
DB 1077 TAAAGAAATGTTGATTTGTTAATAGTCAATGATTTTCTTAAGAAAGTGTGTTGGT 1136
QY 1286 TCTCCAGCTTGTGGGTGTGCAAGCAAAAGGATGTTTGAATTAAGATGAGTGAAGTG 1345
DB 1137 GCGAGATCTTGTGGGTGAGAGAAACAAAGACTGATCAAGAACAAAGATGATGATG 1196
QY 1346 GGTGTTGCTCTCTGAGAAATCTTACTCTGAATT 1384
DB 1197 GGTCTTGTCTCCGTTGAAGAAACCTGTACTGAATT 1235
RESULT 4
ADU20461
ID ADU20461 standard; cdNA; 1239 BP.

XX	
AC	ADU20461;
XX	
DT	13-JAN-2005 (first entry)
XX	
DE	A. thaliana drought tolerance-associated cDNA At2g42690.
XX	
KW	s8; gene; plant; tolerance; resistance; environmental stress; drought.
XX	
OS	Arabidopsis thaliana.
XX	
PH	Key Location/Qualifiers
FT	1..1239
FT	/tag= a
FT	/product= "drought tolerance-associated protein"
PN	WO2004092349-A2.
XX	
PD	28-OCT-2004.
XX	
PZ	15-APR-2004; 2004WO-US011887.
XX	
PR	15-APR-2003; 2003EP-00008079.
PR	01-AUG-2003; 2003EP-0001671.
XX	
PR	30-SEP-2003; 2003EP-00022226.
XX	
PA	(BADI) BASF PLANT SCI GMBH.
XX	
PI	Puzio P, Chardonnens A, Chen R, Puente P;
DR	WPI; 2004-766856/75.
XX	
DR	P-P5DB; ADU20462.
PT	
PT	New transformed plant cell with altered metabolic activity compared to a
PT	corresponding non transformed wild type plant cell, useful for producing,
PT	screening and breeding plants with increased tolerance to environmental
PT	stresses.
PS	
PS	Disclosure; SEQ ID NO 107; 607pp; English.
XX	
CC	This invention describes a method resulting in a novel transformed plant
CC	cell which has been altered by an inactivated or down-regulated gene and
CC	results in increased tolerance and/or resistance to an environmental
CC	stress as compared to a corresponding non-transformed wild type plant
CC	cell. The method can be used to generate or screen for seeds or plants
CC	with increased tolerance/resistance to environmental stress and for
CC	detecting stress in cells or plants. The transformed plant cell comprises
CC	a metabolic activity that is altered concerning one or more metabolites
CC	selected from 2,3-dimethyl-5-pyridylquinal, 2-hydroxy-palmitic acid, 3,4
CC	dihydroxyphenyllanolinodopa, 3-hydroxy-palmitic acid, 5-oxoprolin,
CC	alanine, alpha linoanic acid, alpha-tocopherol, aminoadipic acid,
CC	anhydroglucose, arginine, aspartic acid, beta-apo-81 carotenal, serine,
CC	beta-carotene, beta-sitosterol, beta-tocopherol, hexadecatrienic acid,
CC	marginic acid, gamma-aminobutyric acid, (delta-7-cl8,10-cl8) -
CC	hexadecadienic acid, delta-15-cl8-tetracosenic acid, ferulic acid,
CC	carnescentric, cerotic acid (c26:0), citrulline, cryptoxanthine, elicosenoidic
CC	acid (20:1), fructose, fumarate, galactose, gamma-tocopherol, gluconic
CC	acid, glucose, glutamic acid, glutamine, glycerate, glycerinaldehyde,
CC	glycerol, glycerol-3-phosphate, glycine, homoserine, inositol,
CC	isoleucine, iso-maltose, isopenentyl pyrophosphate, leucine, lignoceric
CC	acid (c24:0), linoleic acid (cl8:2 (c9, cl2)), lutene, lycopen, malate,
CC	mannose, methionine, methylgalactopyranoside, methylgalactopyranoside,
CC	methylgalactopyranoside, palmitic acid (cl6:0), phenylalanine, phosphate,
CC	proline, putrescine, pyruvate, raffinose, ribonic acid, shikimate,
CC	sialinic acid, stearic acid (cl8:0), succinate, sucrose, threonine,
CC	tetraoctanoic acid, triphophane, tyrosine, ubiquinone, udc-glucose,
CC	valine, and zeaxanthine. The plant is selected from maize, wheat, rye,
CC	oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
CC	maihot, pepper, sunflower, flax, borage, safflower, linseed, primrose,
CC	rapeseed, turnip rape, vagetes, solanaceous plants, potato, tobacco,
CC	eggplant, tomato, Viola species, pea, alfalfa, coffee, cacao, tea, Salix
CC	species, oil palm, coconut, perennial grass, forage crops and Arabidopsis
CC	thaliana. The environmental stress is selected from salinity, drought,

Query Match	22.9%	Score 351.4	DB 13	Length 1239
Best Local Similarity	57.9%	Pred. No. 3.7e-73		
Matches	752	Conservative	0	Mismatches 466; Indels 81; Gaps 4
QY	89	CCCAACATGCGCCGAACTCTCGGGTCCAAATGCTTTGGCGGGCTACTAAACCCGCTCAA	148	
DB	15	CACATCATGGGAAAGAACTCTTAGGCTCAAGAAATTTGGGACATCTATTAGACCCATTAGA	74	
QY	149	CGATAGAGTCCGTGAGCTCCCTCCCTTAAGCGTGGGGGACCTTTCGCGAGTGACATTAAGAC	208	
DB	75	CCAATCACTTAGGGAACCTCATCTTACGTGTGGCGACATTTGTCAAGCCACCTACAGATGC	134	
QY	209	CTTCATTAAGACACCAAGACTCGTCTACTTGGCGGACAGCCGCTACGGGAAGCGGACCT	268	
DB	135	CTTGCTCAACGACCAAACTCCAAATACTGTGGAGCCAGCCGCTACGGCAATCTTTCTTT	194	
QY	269	ACTTCATTAAGACCCGCTTCCGGGGGGGCGAGACCGGTTTGAAGTGGTGGCGCTACTTGTGA	328	
DB	195	CTTGACAGAAAG---GTCATGCTCGAAGAAAGCCTTCGAGTACGAGGTGTGAATCTTCTCTA	251	
QY	329	CGCCACTGCGAAGGTCACAGCTGCCACTTGGCGGACAGCCGCTACGGGAAGCGGACCT	388	
DB	252	CGCCACACCTCGTGTCTCTCTCCCGAAGGTTTGTCTTCCAAATACAAATCAAGAGATTTC	311	
QY	389	GTGGGATTTGGGAATGAATTTGGATTTGGGTATGTCTGTGTGTAATGACGACAGTGC	448	
DB	312	TTGGGACCGTGAAGTTAACTGTTGGCTTCACTTCTGTCAAGTCTGATGAACGGTCTAA	371	
QY	449	GATGCGGGACGAAAGGAGGTGTATGTGTGTGAGAGGGAATTGAGGATTTATGATG	508	
DB	372	GACTTTAGAGCGCGGTGATCTATATATAGCTTTGAGAGGAAGACAGACGAACTATGATAGTG	431	
QY	509	GATTGATGTTCTTGTTGCTCAACTTTGAAGTCTGCTATCTTTGTTATGCGACTCAACAAAC	568	
DB	432	GATCATGTTTGGGTGTCTAGGCCCAACTTCAGCTACCCCTTGTCTGACGGAACCCGAGCA	491	
QY	569	TATCATGTTGAAAAGTGTGAAAATGAGAGAAAAGAAAGACATTCAATAATCAAGTTGTGA	628	
DB	492	GGATGTTCTGGTGTGATGTTGAA-----GGTA	520	
QY	629	CGACTGTTTCAATATCAACTTACTAGTTTCCGCGCTCAAGACAAAGAAAAGAAAGCA	688	
DB	521	CGACTTT-----GATAGTGA	536	
QY	669	CGACGACGATATGACGACCCCAAGATGATGCAAGTTGGATGACAAATATACATTCGGA	748	
DB	537	CAGTGAAATGAAGAAAGGTGTAAAGTATGCTCGGGTGGCTCACAAACTTATATCTTAA	596	
QY	749	GGATCCCAATACCCCTTCAAAAATTAAGTGCAAGAACACAACTTCAGACCAAACTCAA	808	
DB	597	TCACCCCGAATGAAATATCACTAAGCTAAGTCTAGGTCACAGTTGTTAGCCAAAGATCA	656	
QY	809	ACAACTATGACAAATATCAAAAGCGAAACCTTAGCATTAACATTCGCGCGTCAAGCT	868	
DB	657	GGAGTTCTGTGAAGTATTAAGAGACGAAGAACGACATTTGTGTTGACGTGACATAGCTT	716	
QY	869	AGGCGCGACACTATCATGCTGTAGCGCTTGACACTATGTGAGAA---TCTCAGACCGA	925	
DB	717	GGAGAGCTACAAAGGCTGTTTGGCGCGCTAATGATTTACTGTGAACGGTTCCAGATGATGA	776	

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QY 926 GATCCAGTCAAGCCGCTGCTTCCGGTCCCAAAAGTAGCAACAATAATTCACA 985
DB 777 TGTTCGGCTCACTCTATAGTCTTGGTGTCCACAGTATAGAAACAAAGGTTCAAGA 836
QY 986 ACTCTTGACTCGTACCCAAACCTAAATGTCCTCCATGTAAAGAAATGCATGACTGAT 1045
DB 837 CGAAGTATAGTACAAAGAACTTAAGATCCTCCATGTAAAGAAACGATTTGATCTCTT 896
QY 1046 CCGCTGTATCCGTGAAACCTCATAGGTTACGTGAACCTTAGAATCCAGCTGGAGATCGA 1105
DB 897 AACTCGATACCCAGGGGACTTTAGGGTATGTGACCTAGAAATAACTTTGATCGA 956
QY 1106 CTGAGGAAGTCGACCTTTCTAAAGACTCGAAAAACCGAGTATGGCATTAATTTGCA 1165
DB 957 TACAAAGAGTACACCGTTCTTAAGGATTCAAAGAAATCCAGGATTTGGCATTAATCTTCA 1016
QY 1166 AGCAATATTCGATGTTTGAAGTGTGGCATGGGGTTAAGGGGAGTTAAAGTTGTTAA 1225
DB 1017 GGGGATGTATCATGTTGTAGCTGATGGAATGGGAAGAAAGAGTTTAAACTGATGCT 1076
QY 1226 TAAAGAAAGTGTGCTGTTGTTAATTAATCATGTGATTTTCTTAAGAAAGATGTTGCT 1285
DB 1077 TAAAGAAAGTATTCGATTAAGTGAACAAAGTCAATGCGAGTTCTTGAAAGCTGAGTGTGGT 1136
QY 1286 TCCCTCCAGCTTGTTGGGTTGTGCAAGAACAAAGGATGGTTTGAATTAAGATGTGAGTG 1345
DB 1137 GCCAGGATCTTGTTGGGTTAGAGAAAGAACAAAGGACTGATCAAGAAAGAAATGTGATG 1196
QY 1346 GGTTCCTGCTCTCTCTGAGGAAGATCTACTCTGTAAT 1384
DB 1197 GGTTCCTGCTCTCTCTGTAAGAAAGAACTGTACTGTAAT 1235

RESULT 5
ADU20618
ID ADU20618 standard; DNA; 1239 BP.
XX
AC ADU20618;
DT 13-JAN-2005 (first entry)
DE A. thaliana At2g42690 homologue DNA.
XX
KM gene; plant; tolerance; resistance; environmental stress; drought; ds;
KM lipase.
XX
OS Arabidopsis.
OS thaliana;.
XX
FH
FT Key Location/Qualifiers
FT CDS 1..1239
FT /tag= a
FT /product= "putative lipase"
PN WO2004092349-A2.
XX
PD 28-OCT-2004.
XX
PF 15-APR-2004; 2004WO-US011887.
XX
PR 15-APR-2003; 2003BP-00008079.
PR 01-AUG-2003; 2003BP-00016671.
PR 30-SEP-2003; 2003BP-00022226.
XX
PA (BAD1 ) BASF PLANT SCI GMBH.
PI Puzio P, Chardonens A, Chen R, Puente P;
DR WPI, 2004-766856/75.
DR P-PSDB; ADU20619.
XX
XX New transformed plant cell with altered metabolic activity compared to a

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PT corresponding non transformed wild type plant cell, useful for producing,
PT secreting and breeding plants with increased tolerance to environmental
PT stress.

PS Disclosure; Page 579; 607pp; English.

XX This invention describes a method resulting in a novel transformed plant
CC cell which has been altered by an inactivated or down-regulated gene and
CC results in increased tolerance and/or resistance to an environmental
CC stress as compared to a corresponding non-transformed wild type plant
CC cell. The method can be used to generate or screen for seeds or plants
CC with increased tolerance/resistance to environmental stress and for
CC detecting stress in cells or plants. The transformed plant cell comprises
CC a metabolic activity that is altered concerning one or more metabolites
CC selected from 2,3-dimethyl-5-phytylquinol, 2-hydroxy-palmitic acid, 3,4
CC dihydroxyphenylalanine, 3-hydroxy-palmitic acid, 5-oxoprolin, 3,4
CC alminic, alpha linolenic acid, alpha-tocopherol, aminoaliphatic acid,
CC anhydrotolucene, arginine, aspartic acid, beta-apo-81 carotenal, berine,
CC beta-carotene, beta-sitosterol, beta-tocopherol, hexadecatrienic acid,
CC margaric acid, gamma-aminobutyric acid, (delta-7-cis,10-cis)-
CC hexadecadienic acid, delta-15-cis-tetradecenoic acid, ferulic acid,
CC campesterol, cerotic acid (c26:0), citrulline, cryptoxanthine, eicosenoic
CC acid (20:1), fructose, fumarate, galactose, gamma-tocopherol, gluconic
CC acid, glucose, glucamic acid, glutamine, glycerate, glycerinaldehyde,
CC glycerol, glycerol-3-phosphate, glycine, homoserine, inositol,
CC isoleucine, iso-maltose, isopentenyl pyrophosphate, leucine, lignoceric
CC acid (c24:0), linoleic acid (c18:2 (c9, c12)), luteine, lycopene, malate,
CC mannose, methionine, methylgalactofuranoside, methylgalactopyranoside,
CC methygalacturonoside, palmitic acid (c16:0), phenylalanine, phosphate,
CC proline, putrescine, pyruvate, raffinose, ribonic acid, shikimate,
CC sinapine acid, stearic acid (c18:0), succinate, sucrose, threonine,
CC triacontanoic acid, tyriophane, tyrosine, ubiquinone, udp-glucose,
CC valine, and zeaxanthine. The plant is selected from maize, wheat, rice,
CC oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
CC manihot, pepper, sunflower, flax, borage, safflower, linseed, primrose,
CC rapeseed, turnip rape, legumes, solanaceous plants, potato, tobacco,
CC eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix
CC species, oil palm, coconut, perennial grass, forage crops and Arabidopsis
CC thaliana. The environmental stress is selected from salinity, drought,
CC temperature, metal, chemical, pathogenic and oxidative stresses, or their
CC combinations. The inactivation or down-regulation of the gene is achieved
CC by double-stranded RNA interference (dsRNA), introduction of an
CC antisense nucleic acid, a ribozyme, an antisense nucleic acid combined
CC with a ribozyme, a nucleic acid encoding a co-suppressor, a nucleic acid
CC encoding a dominant negative protein, DNA- or RNA- or protein-binding
CC factors targeting said gene or -RNA or -protein, RNA degradation
CC inducing viral nucleic acids and expression systems, systems for inducing
CC a homolog recombination of the genes, mutations in the genes or their
CC combinations. This sequence represents a homologue of an Arabidopsis
CC thaliana drought tolerance gene.

XX Sequence 1239 BP; 346 A; 249 C; 323 G; 321 T; 0 U; 0 Other;

Query Match 22.9%; Score 351.4; DB 13; Length 1239;

Best Local Similarity 57.9%; Pred. No. 3.7e-73;

Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;

```

QY 89 CCCAAGATGGCCGAGACTCCGAGGTCCAAATGCTTGGCGCGGCTACTTAAACCGCTCAA 148
DB 15 CACATCATGGAGAAAGAACTTTAGGCTCAAGAAATTTGGACACTATCTTAGACCACTTGA 74
QY 149 CGATGAGCTCCGTGAGCTCTCTACGCTGGGGGACTTTCGACAGTAGACATAGACAG 208
DB 75 CCAATCATTTAGGGAAGCACTTACGTGTGGGACTTTGTCAAGCACACTAGAGATG 134
QY 209 CTTCTATAAGACAGCAAACTGCTCTATCTGGGCGACGCGGCTTACGGGAAGCGGAGACT 268
DB 135 CTTGCTCAAGACCAAACTCCAAAGTACTGTGGAGCCGCGGCTTACGGCAATCTTCTTT 194
QY 269 ACTTCATAAGACCGGCTCCGGGGGGGCGAGACCGGTTTGACGTTGAGGCTACTTGTGA 328
DB 195 CTTGCAAG--GTCATGTCGAAAAAGCTTCCGACTTACGAGGTTGTAACTTCTCTTA 251

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QY 329 CGCCACTCGAAGGTCAAGCCGTCAGAGCCGTTCTGCTGAAGTCGAGTCGAGGAGAA 388
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Db 312 TTGGGACCGGAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 371
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QY 449 GGTGGCGGAGCGAAGGGAGGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 508
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Db 372 GGCCTTAGAGACCGCTGAGATCTATATAGCTTTAGAGAGAAAGAGAGAGAGATGATG 431
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QY 509 GGTGATGTTCTTGCTGCTCAACTTGAAGTCTGCTCATCTTTGTTAGCACTCAACAAC 568
| | | | |
Db 432 GGTCAATGTTTGGGTCTAGGCCAAGCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 491
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Db 492 GGAATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 520
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QY 629 CGACTGTTCAATATCAACCTACTAGGTTCCGCTCCAAAGCAAGAAAAGAGAGCGA 688
| | | | |
Db 521 CGACTTTT-----GATAGTGA 536
| | | | |
QY 689 CGACGACGATGATGACGACCCCAAGTGAAGCAAGTTGATGACAAATATACATCGGA 748
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| | | | |
QY 1046 CCTCTGTATCCGCTGAACCTCATGGGTTACGTGAACATAGGAATCGAGCTGAGATCGA 1105
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Db 1137 GCGAGAGATTTGGGTGAG 1196
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QY 1346 GGTTCGCTGCTTCTGAGAGAGATCTTACTCTGCAATTT 1384
| | | | |
Db 1197 GGTTCGCTGCTTCTGAG 1235
| | | | |

RESULT 6
AAC42410
ID AAC42410 standard; DNA; 1259 BP.
XX
AC AAC42410;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 35449.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
KM protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
EN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
XX
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128224P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132464P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 16-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138847P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
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PR 18-JUN-1999; 99US-0139454P.
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PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.

PR 18-JUN-1999; 99US-0139459P.
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
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PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
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PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141847P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145219P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148311P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.

PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152633P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
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PR 14-OCT-1999; 99US-0159329P.
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PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161923P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 22.9%; Score 351.4; DB 3; Length 1259;
Best Local Similarity 57.9%; Pred.No.3.7e-73;
Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;

QY 89 CCACATGCGCCGAACCTCTCGGGTCCATGCTTGGCGCGGACTTCTGCAAGTGAACACCGCTCA 148
DB 35 CACATCATGGAGAAGAACCTTAAAGCTCAAGATTGGGACACTATCTTAAGCCATTGA 94
QY 149 CGATGAGCTCCGTGAGCTCTCTAAGCTGCGGGGACTTCTGCAAGTGAACACCGCTCA 208
DB 95 CCAATCACTTAGGGAATCAATCTTACGTTGATGGCGACTTTGTCAAGCCACTACGATGC 154
QY 209 CTTCAATAACGACCAAGACTGTCCTATGCGGCGACGCCGCTACCGGAAGCGGAGCT 268
DB 155 CTTGCTCAACGACCAAACTCAAGTACTGTGAGCCGCGCTACGGCAATCTTCTTT 214

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Qy 269 ACTTCATTAAGACCCGCTTCCGCGGGGGGCGACACCGGTTTGACGTGCGGTACTTGTGA 328
Db 215 CTTCGACAGAG---GTCAATGCTCGAAAAAGCTTCCGACTACAGAGGTGTAACCTTCCTCTA 271
Qy 329 CGCCATGCGAAGGTCAAGCGTCCGAGAGGCGTTTCTGCTGAAGTCGAGTCGAGGAGAA 388
Db 272 CGCCACAGCTGCTGTTTCTCTCCCGAAGGTTTCTTCCAAATCACAATCAAGAGATTC 331
Qy 389 GTGGAGTAAGGAAATCGAATTGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 448
Db 332 TTGGAGCCGTGAAGTCTTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 391
Qy 449 GGTGGCGGAGCGAAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 508
Db 392 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 451
Qy 509 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 568
Db 452 GGTCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 511
Qy 569 TACTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 628
Db 512 GGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Qy 629 CGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 688
Db 541 CGACTTTT-----GATATGTGA 556
Qy 689 CGACGACGATGATGACGACCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 748
Db 557 CAGTGAAGATGAAGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 616
Qy 749 GGATCCCAATCACCCTTCAAAAATCTAAGTCAAGAACAACTTCAAGCAAACTCA 808
Db 617 TCACCCCGAATCGAATCTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 676
Qy 809 ACACTATATGCAAAATTCAGAAAGCAAAACCTTAAGCAATATTCGCGGTGTGTGTGT 868
Db 677 GGAAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 736
Qy 869 AGGCGGACACTATCAGTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 925
Db 737 GGGAGCTACAGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 796
Qy 926 GATCCCACTGACGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 985
Db 797 TGTTCCTGCTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 856
Qy 986 ACTCTTGACCTGTACCAAACTTAATGTCTCATGTATGAAGTGTGTGTGTGTGTGT 1045
Db 857 CGAAGTATAGTACAGAAAGCTTAAGATCTTCATGTAAAGAAACGATTTGATCTTT 916
Qy 1046 CCGCTGTATCCCGTGAAGCTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1105
Db 917 AACTCGATACCAAGGGGACCTTTAGGTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 976
Qy 1106 CTGAGGAAGTGCACCTTTCTTAAGAGACTGCAAAAACCCGAGTATGTGTGTGTGT 1165
Db 977 TACAAAAGAGTCAACGCTTCTTAAGCGATTCAGAGAAATCAAGGAGATTGGCATTAATCTTCA 1036
Qy 1166 AGCAATATGTGATTTGTGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1225
Db 1037 GGGCATGTATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1096
Qy 1226 TAAAGAGAAGTGTGCATTTGTAAATAGTCATGTGATTTTCTTAAGGAAGATTTGTGT 1285
Db 1097 TAAAGAGAAGTATTCATTAAGTGAACAAGTCAATGAGTCTTGAAGTGTGTGTGTGT 1156
Qy 1286 TCCTCCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1345
Db 1157 GCCACGAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1216
Qy 1346 GGTTTTGGCTCTCTAGAGAAATCTTACTCTGGAAT 1384

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Db 1217 GGTTCCTTCCTCCGTTGAAGAGAACTGTACTGGAAT 1255
RESULT 7
AAAS3885
ID AAAS3885 standard; DNA; 1167 BP.
XX
AC AAAS3885;
XX
DT 03-JAN-2001 (first entry)
XX
DE Arabidopsis EST showing 55/5% homology with senescence induced.
XX
KM Senescence-induced lipase; senescence; lipase; antisense; regulation;
XX modulation; resistance; stress; crop protection; ethylene; ds.
XX Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 1..1047
FT /*tag= a
FT /label= EST
XX
PN MO200049164-A1.
XX
PD 24-AUG-2000.
XX
PE 14-FEB-2000; 2000MO-US003494.
XX
PR 16-FEB-1999; 99US-00250280.
XX
PA (SENESC-) SENESCO INC.
XX
PI Thompson JE, Wang T, Hudak K, Hong Y,
XX
DR WPI: 2000-549277/50.
XX P-PSDB: AAY97308.
XX
PT DNA encoding carnation senescence-induced lipase, useful for regulating
PT the expression of senescence in plants to delay its onset and improve
PT plant resistance to environmental stress, thus extending shelf-life or
PT growth period.
XX
PS Disclosure; Fig 13; 89pp; English.
XX
CC Insertion of the senescence-induced lipase coding sequence in an
CC antisense direction in a plant genome can be used to regulate the
CC expression of senescence in those plants. Alteration of expression of the
CC senescence-induced lipase gene in plants results in delayed onset of
CC senescence and improved resistance to environmental stress, thus
CC extending the plant shelf-life and/or growth period. The genetically
CC altered plant is useful for producing a new variety or line of plants
CC where the alteration is stably transmitted from generation to generation.
CC This method of regulation is advantageous over prior senescence
CC modulating technologies since prior methods were only applicable to a
CC limited range of plants, e.g. to plants that are ethylene-sensitive. The
CC antisense regulation method is applicable to all types of plants,
CC regardless of ethylene sensitivity
XX
SQ Sequence 1167 BP; 338 A; 213 C; 305 G; 311 T; 0 U; 0 Other;
Query Match 18.9%; Score 291.2; DB 3; Length 1167;
Best Local Similarity 64.3%; Pred. No. 7.4e-59;
Matches 453; Conservative 0; Mismatches 248; Indels 3; Gaps 1;
Qy 684 AGGAGAGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 743
Db 340 AGTACAGTGAAGTGAAGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 399
Qy 744 TCGGAGATCCCAATCAACCTTCAAAAATTAAGTCAAGAACACAACTTCAGACCAAA 803
Db 400 TCTAATCAACCCGATGTGAATTCATTAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 459

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QY 1281 TTGGTTCCTCCAGCTTGGTGGTGTGTGAGAACAAAGGATGTTTGAATPAAGATGCT 1340
 |||||
 DB 940 TTGGTTCGACAGATCTTGGTGGGTAGAGAAACAAAGACTGACAAAGAAAGATGCT 999
 |||||
 QY 1341 GAGTGGGTTTGGGCTCTCTCTGAGGAAGATCTTACTCTGAATT 1384
 |||||
 DB 1000 GAATGGGTTCTTGGCTCCCGTTGAAGAAACCTGTACTGAATT 1043
 |||||

RESULT 9
 ACL26423
 ID ACL26423 standard; cDNA; 1077 BP.
 AC126423;
 XX
 AC 02-JUN-2005 (first entry)
 XX
 DT Rice abiotic stress responsive polynucleotide SEQ ID NO:379.
 XX
 DE ss; abiotic stress tolerance; transgenic plant; plant; cereal;
 KM agriculture.
 XX
 OS Oryza sativa.
 XX
 PN WO2003008540-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-US019668.
 XX
 PR 22-JUN-2001; 2001US-0300112P.
 XX
 PR 24-AUG-2001; 2001US-0314662P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 21-NOV-2001; 2001US-0332132P.
 XX
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA
 PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
 PI Moughamer T, Provart N, Rieke D, Zhu T;
 XX
 DR WPI; 2003-248011/24.
 XX
 PT New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.
 XX
 PS Claim 1; SEQ ID NO 379; 899p; English.
 XX
 CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention

QY 693 GACGATGATGACGACCCCAAGTATGCAAGTTGATGACAAATATACATCGAGAGAT 752
 |||||
 DB 397 GGCAGTCTGATGACCTTGTGTGCATGGGGGGTGGCTGTCTGTGTACACGAGTCCGAT 456
 |||||

Query Match 11.0%; Score 169.4; DB 11; Length 1077;
 Best Local Similarity 55.2%; Pred. No. 6.6e-30;
 Matches 376; Conservative 0; Mismatches 296; Indels 9; Gaps 2;

QY 753 CCCAATACCCCTTCCAAAACTAAGTGACAGAACACAACTCTCAGACCAACTCAAA 812
 |||||
 DB 457 CCAAGATCTCAGTACAAATTAAGAGAGTGCAGAGATATCAGGCTTGAATGAGATCAAAACGG 516
 |||||
 QY 813 CTAATGACAAATATCAAAAGACGAAACCTTAAGCTAATCTTCCGGGTCAAGCTTAGGC 872
 |||||
 DB 517 CTCGAGATATGTACGAGCATGAGAGACTAGCATCAACATTAAGGACCAAGCTTGGG 576
 |||||
 QY 873 GCGACATATCAGTCTGAGGCGCTTGCACATAGTGGAGATCTCAAGACCGAGATC--- 929
 |||||
 DB 577 GCTGCACCTTGGCACCATCAATATGCACTGACATTTGTCTTCAATGGTTACACAAAGCTGT 636
 |||||
 QY 930 CCAATCAAGCGCGGTGTCTTCCGGTGGCCAAAGTAGGCAACAAAAATTCACAACTC 989
 |||||
 DB 637 CCAATGTCTGCTTGGCTTCTTGGTAGCCCAAGAGTGGGCAACCTGATTTTCAAAAGCG 696
 |||||
 QY 990 TTGCATCTGTAACCAACCTTAATGTCTTCAATGTAAAGAAATGATCATGACCTGATCCT 1049
 |||||
 DB 697 TTGCACATGTCTCCAGATTTGAGATTGCTCCGCAATGAAAATCTCTCGATGTGATCCA 756
 |||||
 QY 1050 CTGTATCCCGTGAACATCATGGGTTAGTGAACATAGGAATCGAGCTGAGATGACTCG 1109
 |||||
 DB 757 AACTGGCC-----AAACTAGATACAGGATGCTGGCACAGAGCTGATGATGATACA 810
 |||||

QY 1110 AGGAATGCACTTTCTTAAAGAACTCGAAAAACCCGATGTTGGCAATATTTGCAAGCA 1169
 |||||
 DB 811 GGGAAATCACCATATCTGAAAGGCCCTTGGGAATCTCTTAACGTGGCATGATGAGATGC 870
 |||||
 QY 1170 ATATGCAATGTTGTAAGTGTGGCATGGGCTTAAGGGGAGTTAAAGTTGTAATPAAG 1229
 |||||
 DB 871 TACATGATGATGGGTTGGCGGGGACGCAAGGAGCAACGAGGGTTCAAGCTGGAATGAT 930
 |||||
 QY 1230 AGAATGTTGATGTTGTTAATTAAGTCAATGATTTTCTTAAAGAAAGATGTTGGTCT 1289
 |||||
 DB 931 CGAACAATGCTTGTGTTTAAACAAACAGAAAGCCACTGAAAGATGATGCAATTTCA 990
 |||||

QY 1290 CCAAGTTGATGGGTTGTGCAAGCAAGAGATGTTTGAATAGATGATGAGGTT 1349
 |||||
 DB 991 TCGTCTTGTGGTGGTGGTGCAGAACAAAGTATGTTGAAGGACAGATGCTGGTGGAT 1050
 |||||

QY 1350 TTGGCTCTCTCTGAGGAAGAT 1370
 |||||
 DB 1051 TTGGCCGACCATGAGATGAT 1071
 |||||

RESULT 10
 ACL26207
 ID ACL26207 standard; cDNA; 1533 BP.
 AC126207;
 XX
 AC 02-JUN-2005 (first entry)
 XX
 DT Rice abiotic stress responsive polynucleotide SEQ ID NO:163.
 XX
 DE ss; abiotic stress tolerance; transgenic plant; plant; cereal;
 KM agriculture.
 XX
 OS Oryza sativa.
 XX
 PN WO2003008540-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-US019668.
 XX
 PR 22-JUN-2001; 2001US-0300112P.
 XX
 PR 24-AUG-2001; 2001US-0314662P.
 XX
 PR 26-SEP-2001; 2001US-0325277P.
 XX
 PR 21-NOV-2001; 2001US-0332132P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
 PI Moughamer T, Provart N, Ricke D, Zhu T;
 XX WPI; 2003-248011/24.
 XX
 PT New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.
 XX
 XX Claim 1; SEQ ID NO 163; 89pp; English.
 XX
 XX The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention
 XX
 SO Sequence 1533 BP; 278 A; 546 C; 463 G; 246 T; 0 U; 0 Other;

Query Match 10.8%; Score 165.6; DB 11; Length 1533;
 Best Local Similarity 54.5%; Pred. No. 6.1e-29;
 Matches 367; Conservative 0; Mismatches 289; Indels 18; Gaps 1;

QY 714 GTGATGCAAGGTGGATGACATATACATCGAGAGTCCCAATTCACCTTCACAAA 773
 DB 709 GTCATGAAGGGGTGTACTCATCTACAGCTCCACCGACAGCGCTCCCTTTCTCCAG 768
 QY 774 CTAAGTGCAAGAACCAACTTCAGACCAACTCAACCACTAATGACAAATACAAAGAC 833
 DB 769 TACAGCGCCCGACCAATGTCGCCCGCGCGAGCTGTGTGCGAGGTACGAGAAC 828
 QY 834 GAAACCTTAAGCATTAATTCGCGGTGACAGCTTACGGCGGACATCTACGTGTAGC 893
 DB 829 GAGAGCCTCGGCGTGTGTCACGCGGGACAGCCTCGGCGGTCCCTGCCACGCTCTGC 888
 QY 894 GCCTTCGACATAGTGGAGAAATCTCAGACCGAG-----ATCCAGTC 935
 DB 889 GCGTTCGATATGTGTGTCAACGCGCTGTCCAAAGTGGCGACGCGCGACATTCGCGTG 948
 QY 936 ACGGCGGTGTCTTGGGTGCCCAAAAGTAGGCAACAAAATTCACCAACTCTTTCGAC 995
 DB 949 ACCGCGGTGTGTTCGGAGCGGACGATCGGGAACCGGAGTTCAAGAGAGATTTCAG 1008
 QY 996 TCGTACCAAACTTAATGTCTTCATGTAAGAAATGTATGACCTGATCCCTGTGAT 1055
 DB 1009 GAGGAGCCCAACTCTCGGCGGTGTGCAAGTCAAGAAATGCCCCGACCTATCCGCTTAC 1068
 QY 1056 CCCGGAATCATGAGGTGTAAGTCAATAGGAATGAGCTGGAGATGACTCGAGAG 1115
 DB 1069 CCGAGCGGCTCTCTGCGTACCGCAACGTGGCAAAACCTTCAGGTGACTTCAAGAG 1128
 QY 1116 TCGACCTTCTTAAAGAGCTCGAAAAACCGAGTGAATTTGGCATTAATTTGCAACAAATATTG 1175
 DB 1129 TCGCCCTTACGTAAACGAGACACCGAGCCAGGCACTACCAACCTCGAGGGAGTCTGA 1188
 QY 1176 CATGTTGAATGAGTGTGGAGTGAAGGGGAGTTTAAAGGTTGAATTAAGAAAGT 1235
 DB 1189 CACACGAGTGGCGGCTGGAAACGGGAAGACGCGAGTTCAAGCTCAGGTGAAGCGCAGC 1248
 QY 1236 GTTGCATGTTTAATTAAGTCAATGATTTCTTAAAGAAAGATGTTGGTTCCTCAGGT 1295
 DB 1249 GTTCGGCTGTGTAAACAAAGTGAAGCGGCTTCTTCAAGGACAGAACCTTGTGCGGAGTGA 1308
 QY 1296 TGGTGGTGTGTCAGAAACAAAGGAGATGTTTGAATTAAGATGTGAGTGGGTTTGGCT 1355

DB 1309 TGGTGGTGTGAGAGAAACAAAGCATGTGTCTGGCCAGAACGGGAGATGGACCTCGAG 1368
 QY 1356 CTTCTGAGGAAGA 1369
 DB 1369 GGGCCCGCAGAGGA 1382

RESULT 11
 ADA71310
 ID ADA71310 standard; DNA; 2064 BP.

AC ADA71310;
 XX 20-NOV-2003 (first entry)
 XX
 DE Rice gene, SEQ ID 4633.

XX plant; bacterial infection; fungal infection; viral infection; rice;
 KW gene; ds.

XX Oryza sativa.

XX W02003000898-A1.

XX 03-JAN-2003.

XX 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,
 PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX WPI; 2003-175290/17.

PT Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.

PS Claim 6; SEQ ID NO 4633; 89pp; English.

XX The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1
 CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.

SEQ Sequence 2064 BP; 423 A; 644 C; 624 G; 373 T; 0 U; 0 Other;

Query Match 10.8%; Score 165.6; DB 8; Length 2064;
 Best Local Similarity 54.5%; Pred. No. 6.8e-29;
 Matches 367; Conservative 0; Mismatches 289; Indels 18; Gaps 1;

QY 714 GTGATGCAAGGTGGATGACATATATACATCGAGAGTCCCAATTCACCTTCACAAA 773
 DB 1240 GTCATGAAGGGGTGTACTCATCTACAGCTCCACCGACGAGCGCTCCCTTTCTCCAG 1299
 QY 774 CTAAGTGCAAGAACCAACTTCAGACCAACTCAACCACTAATGACAAATTAACAAAGAC 833
 DB 774 TACAGCGCCCGACCAATGTCGCCCGCGCGAGCTGTGTGCGAGGTACAGGAAC 1359
 QY 834 GAAACCTTAAGCATTAATTCGCGGTGACAGAGCTTACGGCGGAGACATCTACGTGTAGC 893
 DB 1360 TACAGCGCCCGACCAATGTCGCCCGCGCGAGCTGTGTGCGAGGTACAGGAAC 1359
 QY 834 GAAACCTTAAGCATTAATTCGCGGTGACAGAGCTTACGGCGGAGACATCTACGTGTAGC 893
 DB 1360 GAGACCTTCGCGGTGTGTGACAGCGGAGCAAGCCTTCGCGGTGTGCGACCGCTTGC 1419

QY 894 GCCTTCACATAGTGAGAAATCTCACGACCGAG-----ATCCCAATC 935
 DB 1420 GCGTTCATATCGTCGTCAACGCGGTGTCCAGAGTCGCGCCAGCGGCACATCCCGGTG 1479
 QY 936 ACCGCGGTGTCTTTCGGGTGCCCAAAAGTAGGCAACAAAATTCCAACTCTTCGAC 995
 DB 1480 ACCCGCGGTGTCTTTCGGGTGCCCAAGTCCGGAACCCGAGGTTCAAGAAAGCACTTCGAG 1539
 QY 996 TCGTACCCAAACCTAAATGTCTTCATGTAGGAATGCAATCGAAGCTGATCCCTGTAT 1055
 DB 1540 GAGCAGCCCAACCTGCGGCGCTGACGTCAAGAAATGCCCCGACCTCATCCGCTCTAC 1599
 QY 1056 CCCGTGAACCTCATGGGTTCAGTGAACATAGAAATCGAGCTGAGATCGACTCGAGAAG 1115
 DB 1600 CCGAGCGGCTCTCTCCGCTAGCCCAAGTCCGCAAAACCTCCAGGTGACTCCAAAGAG 1659
 QY 1116 TCGACCTTTCTTAAAGACTCGAATAACCCGAGTATGGCATTAATTGCAAGCAATATG 1175
 DB 1660 TCGGCTTACGTGAAGCGAGACACAGCCCAAGCGACTCAACAACTGCAAGGGATCCTA 1719
 QY 1176 CATGTTGTAAGTGTGGTTCATGGGTTAAGGGGAGTTTAAGTTGTAATTAAGAAAT 1235
 DB 1720 CACACGCTGCGCGCTGGAACGGAAGACGCGCAAGTTCACAGTGAACGCGAGC 1779
 QY 1236 GTTGCATTGTTAATAGTCAATGATTTTCTTAAAGAAAGAAATGTTGTTCTCCAGCT 1295
 DB 1780 GTCCCGCTGTGAACAAATGTCAGCGGCTTCTCAAGGACAGCAACTTGTCCGAGTCA 1839
 QY 1296 TGGTGGTGTGTGCAAAACAAAGGATGTTTGAATAGATGAGTGGTGGTGGTCT 1355
 DB 1840 TGGTGGTGTGAGAGGAACAAAGCATGCTGCTCGGCCAAGACGGGAATGCACTCGAG 1899
 QY 1356 CCTCTTGAAGAA 1369
 DB 1900 GGGCCCCGACAGGA 1913

RESULT 12

ADK60584
 ID ADK60584 standard; cDNA; 1384 BP.

AC ADK60584;

DT 21-APR-2005 (first entry)

DE Plant full length insert polynucleotide seqid 31427.

XX plant protectant; plant growth regulant; gene therapy; plant;

KM recombinant DNA construct; physical array; plant breeding marker;

KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

KM extreme osmotic condition; pathogen tolerance; pest tolerance;

KM growth rate; cell cycle pathway; disease resistance;

KM galactomannan production; lignin production; plant growth regulator;

KM yield; plant growth; plant development; seed oil; protein yield;

KM protein content; gene; ss.

XX unidentified.

OS US2004034888-A1.

PN US2004034888-A1.

PD 19-FEB-2004.

XX 28-APR-2003; 2003US-00425114.

XX 06-MAY-1999; 99US-00304517.

PR 05-NOV-2001; 2001US-00385678.

XX (LIU/J) LIU J.

PA (ZHOU/J) ZHOU Y.

PA (KOVA/J) KOVALIC D K.

PA (SCRE/J) SCREEN S E.

PA (TABAK/J) TABASKA J E.

PA (CAO/J) CAO Y.
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI
 XX WPI: 2004-180133/17.
 DR
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX
 XX Claim 1; SEQ ID NO 31427; 15pp; English.
 PS
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspro.gov/sequence.html?docid:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 1384 BP; 352 A; 330 C; 408 G; 294 T; 0 U; 0 Other;

Query Match 9.8%; Score 151; DB 13; Length 1384;
 Best Local Similarity 53.8%; Pred. No. 1,7e-25;
 Matches 363; Conservative 0; Mismatches 300; Indels 12; Gaps 2;

QY 702 GAGACCCCAAGATGATGCAAGTGGATGCAATATACATCGAGATCCCAATCA 761
 DB 556 GCCAACCCCTGTGTGATGAGAGGTGGCTTTCAGTCTACAGAGTGTGATCCAGGGTCA 615
 QY 762 CCCCTGACAAATCTAATGTGCAAGAACCACTTCAAGCAAACTCAATATGACA 821
 DB 616 CAGTACAAACAAAGAGACCGCAAGCATCAAGTGTAAACGAGTGAAGAAAGATACAGAT 675
 QY 822 AATACAAAGACGAACCTTAAGCATTAATTCGCCCGGTCAACAGCTAGGCGGACCTA 881
 DB 676 CTGTACAAAGCAAGAGAGAGATCATCATTAACAGGCCACTTAGAGAGCACTT 735
 QY 882 TCACTGTGAGCGCTTTCAGATATG-----GAGAAATCTCAAGACCGAGATCCCATGTC 935
 DB 736 GGCACATCAACGCAACCGCATGCTCTCCAAACGGCTTCAACAGAGACTGTGCTGGTGTG 795
 QY 936 ACCGCGGTGTCTTCCGGGTGCCCAAAAGTAGGCAACAAAATTCACAACTCTTGAC 995
 DB 796 TCGGCTTGTGATTCGAGAGCGCCAGAGTGGAAACCTTGATTTTCCAGAAAGCGCTTGAC 855
 QY 996 TCGTACCCAAACCTAATATGCTTCATGTAAAGATGATCACTGATCCCTGTAT 1055
 DB 856 AGCGCGGCGGACCTGAGAGTGTCTCCGGTCCGAACTCTCCGACGTGTCCCAATGG 915
 QY 1056 CCGGTGAACCTCATGGTGTAGTGAACATAGAAATGAGCTGAGATGCAAGAG 1115
 DB 916 CCAAG-----CTAGGGTACAGTATGTGCGCACAGAGCTGATGATGACAGAGAA 969
 QY 1116 TCGACCTTCTTAAAGACTGGAATAACCCGAGTATGGCATTAATTGCAAGCAATATG 1175
 DB 970 TCGGCTTACCTGAAGGCGCTTGAAGACCCCTGACATGCAATGATGAGTGTATCATG 1029
 QY 1176 CATGTTGTAAGTGTGGCATGAGGTTAAGGGAGATTAAAGTTGTAATTAAGAAAT 1235
 DB 1030 CACGGGTGCTGTGGGTCAAGGGGAGAGAGGTTGACAGCTTGTGTGATCGGGAC 1089

Oy		1236 GTTGCAATTGGTTAAATAGTCATGTGATTTTCTTAAGAAGAAATGTTTGGTTCCTCCACACT	1239
Dd		1090 GTTGCTTTGGTGAACMACCATGAAAGATCCCTCGAAGAAATGAGTTCCGTGCTCCACCCTGC	1149
Oy		1296 TGGTGGCGTTGTGCAGAACAAAGGCGATGGTTTTGAATAAGCATGTGAGTGGGTTTTTGACT	1355
Dd		1150 TGGTGGGTTGTGTGCAGAACMAAGTATGTGTGAAGCACAAGCATGGCCGGTGCATCTGGCC	1209
Oy		1356 CCTCCTGAGGAAGAT	1370
Dd		1210 GACCATGAGGAGGAT	1224
 RESULT 13			
ID	AAA53884	standard; DNA; 923 BP.	
XX	AA53884;		
XX	03-JAN-2001	(first entry)	
XX		Sensence-induced lipase partial coding sequence.	
DE		Sensence-induced lipase; sensence; lipase; antisense; regulation;	
KW		modulation; resistance; stress; crop protection; ethylene; ds.	
OS		Lycopersicon esculentum.	
FH	Key	Location/Qualifiers	
FT	exon	/tag= a	
FT		//label= Exon 1	
FT	intron	/tag= b	
FT		//label= Intron 1	
FT	exon	/tag= c	
FT		//label= Exon 2	
PN	WO20049164-A1.		
PD	24-AUG-2000.		
Pf	14-FEB-2000; 2000WO-US003494.		
PR	16-FEB-1999; 99US-00250280.		
PA	(SENE-) SENESCO INC.		
PI	Thompson JE, Wang T, Hudak K, Hong Y;		
DR	WPI; 2000-549277/50.		
DR	P-PsDB; AA97303.		
PT		DNA encoding carnation sensence-induced lipase, useful for regulating	
PT		the expression of sensence in plants to delay its onset and improve	
PT		plant resistance to environmental stresses, thus extending shelf-life or	
PT		growth period.	
PS		Disclosure; Fig 10; 89pp; English.	
XX		Insertion of the sensence-induced lipase coding sequence in an	
XX		antisense direction in a plant genome can be used to regulate the	
XX		expression of sensence in those plants. Alteration of expression of the	
XX		sensence-induced lipase gene in plants results in delayed onset of	
XX		sensence and improved resistance to environmental stresses, thus	
XX		extending the plant shelf-life and/or growth period. The genetically	
XX		altered plant is useful for producing a new variety or line of plants	
XX		where the alteration is stably transmitted from generation to generation.	
XX		This method of regulation is advantageous over prior sensence	
XX		modulating technologies since prior methods were only applicable to a	
XX		limited range of plants, e.g. to plants that are ethylene-sensitive. The	

CC	antisense regulation method is applicable to all types of plants,					
CC	regardless of ethylene sensitivity					
XX						
SQ	Sequence	923 BP;	315 A;	148 C;	181 G;	279 T; 0 U; 0 Other;
	Query Match	8.6%;	Score 131.8;	DB 3;	Length 923;	
	Best Local Similarity	58.2%;	Pred. No. 5.5e-21;	Mismatches 177;	Indels 3;	Gaps 1;
	Matches	251;	Conservative 0;			
OY	AAAGACAAAGGAAAAAGGAAGCAGCAGCAGCATGATACGACCCCAAGTATGATCGAAGT	725				
Dd	AAACAACAAGAAGCATGTAGATGAGAGCAGAGCAGGATGATCAAAAGTAATGATGGG	149				
OY	726 TGATGACAATATATACATCGAGGATGCCAAATGCACCCTTCACAAAATTATGTCAGA	785				
Dd	150 TGGCTTAAGATCTACGTCCTCAAGTAAACCCGAAAGTGCTTTTCACGAGACTAAGTCAGA	209				
OY	786 ACACAACTTCGACCAACCACTCAAACAATAATGCAAAATTCAGAAAGCAGAACCCCTAAGC	845				
Dd	210 GAACAACCTTCAGCAAGAAAGATTGAAAGTTAAGAAATGATTAAGATTAAGATTGAGC	269				
OY	846 ATAACTTTCCGCGGTCAAGCCTTAGCGCGCACATATCAGTCGTGAGCGCCTTCGACATA	905				
Dd	270 ATAATCTTTACAGGCAATAGCTCTTGATGCTAGCTTAAGTGTGTTAAGCTTATGATGTG	329				
OY	906 GTGAGAA--TCTCAGACCGAGATCCAGTCAAGCGCGGTGCTTCGGSTGCCAATA	962				
Dd	330 GTTAAATATGCTGTGCGCATTTGATATTCAGTATCTGCAATGTATTTGGTAAGTCACAA	389				
OY	963 GTAGCAACAATAAATTCCAACAACATCTTGCAGCTGTAACCCAACTTAATGTCTCCAT	1022				
Dd	390 GTTGGAAATTAAGCATTTCATTAAGAAAGATCAAGAAATTTCTCAACTTGAATATCTTACAT	449				
OY	1023 GTAAGAAATGTCATCGACCTGATCCCTCTGTATCCCGTGAACATCAAGGTTACGTGAAC	1082				
Dd	450 GTTAAAGAACAAAGATGATCTCATTAACCTTACCAGATGCTGTTGGGTATGTGAT	509				
OY	1083 ATAGGAATCGA 1093					
Dd	510 TCAGGTATTGA 520					
	RESULT 14					
	AAS20753					
ID	AAS20753 standard; DNA; 923 BP.					
XX						
AC	AAS20753;					
DT	09-APR-2002 (first entry)					
XX						
DE	Partial genomic DNA encoding part of tomato senescence-induced lipase.					
XX						
KW	Plant; senescence-induced lipase; regulation of senescence; environmental stress; tomato leaf; gene; de.					
OS	Lycopersicon esculentum.					
XX						
FH	Key	Location/Qualifiers				
FT	CDS	6..921				
FT		/tag= b				
FT		/partial				
FT		/product= "Part of senescence-induced lipase"				
FT		/note= "This sequence lacks both start and stop codons"				
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FT	intron	514..843				
FT		/tag= c				
FT	exon	845..921				
FT		/tag= d				
XX						
PN	WO200198510-A2.					
XX						
PD	27-DEC-2001.					

Db 676 CAGSGCCCACTGATCGGCTACGCGCCGTTTCACCGACGAGACC GCGGCTG 735
Qy 456 GAGCGAAGGAGGCTGTATGCTGTGAGAGGGACTTGTAGGATTAAGTGGT 511
Db 736 GCGCGCGGACATCGCCATCGGCGGCGGACGGTCAAGGAGCTCGAGTGGT 791

Search completed: December 26, 2005, 08:35:02
Job time : 986.564 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 07:08:48 ; Search time 8003.5 Seconds
(without alignments)
10916.277 Million cell updates/sec

Title: US-10-674-540A-1

Perfect score: 1537
Sequence: 1 ggcacgagccatcccaaac.....ctagttcaaaaaaaaaa 1537

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_in: *
3: gb_env: *
4: gb_on: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pr: *
9: gb_ro: *
10: gb_sts: *
11: gb_sy: *
12: gb_un: *
13: gb_vi: *
14: gb_htg: *
15: gb_pl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	100.0	1537	6	ARS76373 Sequence
2	1535.4	99.9	1537	6	BD268753 DNA codin
3	1339.4	87.1	1341	15	AF026480 Dianthus
4	351.4	22.9	1239	6	AX507787 Sequence
5	351.4	22.9	1270	15	AY079356 Arabidops
6	351.4	22.9	1348	15	AY050998 Arabidops
7	291.2	18.9	1167	6	BD268758 DNA codin
8	291.2	18.9	1167	6	ARS76378 Sequence
9	255	16.6	96685	15	AC007087 Arabidops
10	255	16.6	115310	15	AC006931 Arabidops
11	180.2	11.7	1639	15	BT009343 Trilicium
12	167.2	10.9	1805	15	AK098952 Oryza sat
13	165.6	10.8	1810	15	AK104373 Oryza sat
14	165.6	10.8	1810	15	AK106129 Oryza sat
15	165.6	10.8	1921	6	AK069577 Oryza sat
16	165.6	10.8	2064	6	AX654763 Sequence
17	165.6	10.8	110000	15	AP008207_295 Continuation (296
18	165.6	10.8	156850	15	AP002901 Oryza sat

19	139.4	9.1	110000	15	AP008207_262 Continuation (263
20	139.4	9.1	147770	15	AP003792 Oryza sat
21	131.8	8.6	923	6	BD268755 DNA codin
22	131.8	8.6	923	6	ARS76375 Sequence
23	126.8	8.2	119755	14	AP007506 Lotus cor
24	117.6	7.7	110000	15	AP008207_263 Continuation (264
25	117.6	7.7	126195	15	AP003710 Oryza sat
26	117.6	7.6	82594	15	AC005311 Arabidops
27	111.6	7.3	1353	6	AX653421 Sequence
28	110.4	7.2	88352	15	AC105773 Oryza sat
29	110.4	7.2	110000	15	AP008211_187 Continuation (188
30	107.4	7.0	110000	15	AP008211_283 Continuation (284
31	107.4	7.0	119500	15	AC098832 Oryza sat
32	107.4	6.9	187034	15	AC104284 Oryza sat
33	106.2	6.9	1577	15	AK102737 Oryza sat
34	104.6	6.8	1197	6	AX653309 Sequence
35	101.8	6.6	757	15	AB032756 Solanum m
36	101.4	6.6	1400	15	AY085093 Arabidops
37	98.4	6.4	1526	15	AK106659 Oryza sat
38	96.8	6.3	110000	15	AP008211_283 Continuation (284
39	96.8	6.3	119500	15	AC098832 Oryza sat
40	96.8	6.3	187034	15	AC104284 Oryza sat
41	96.6	6.3	48872	15	P9P14 Continuation (264
42	88	5.7	110000	15	AP008207_263 Continuation (264
43	86.4	5.6	1164	6	AX653171 Sequence
44	80.2	5.2	3567	15	AK119380 Oryza sat
45	79.8	5.2	81366	14	AP007690 Lotus cor

ALIGNMENTS

RESULT 1
LOCUS ARS76373 1537 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 1 from patent US 6774284.
ACCESSION ARS76373
VERSION ARS76373.1 GI:56578428
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1537)
AUTHORS Thompson J.E., Wang T.-W., Hudak K. and Hong Y.
TITLE DNA encoding a plant lipase, transgenic plants and a method for controlling senescence in plants
JOURNAL Patent: US 6774284-A 1 10-AUG-2004;
Senesco, Inc.; New Brunswick, NJ
FEATURES
source
1..1537
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 1537; DB 6; Length 1537;
Best Local Similarity 100.0%; Pred. No. 2e-307; Indels 0; Gaps 0;
Matches 1537; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GCACGAGCATTCCAAAGCTCTTACACCACTCAAACTATTCCACATGCTCGACAG 60
Ory 61 CCCAACCTTTAGGCTCTCAAGCGCCGACCAATGCGCGGAAGTCTCTGGGTCATG 120
Db 61 CCCAACCTTTAGGCTCTCAAGCGCCGACCAATGCGCGGAAGTCTCTGGGTCATG 120
Ory 121 CTTGGGCGGGCTACTAAACCGCTCAACGATGAGCTCCGAGACTCTCTACGCTGCG 180
Db 121 CTTGGGCGGGCTACTAAACCGCTCAACGATGAGCTCCGAGACTCTCTACGCTGCG 180
Ory 181 GGAAGCTTCTGCGAGGATGATGACACCTTCATTAAGACAGAACTCGTCTTATGCG 240
Db 181 GGAAGCTTCTGCGAGGATGATGACACCTTCATTAAGACAGAACTCGTCTTATGCG 240

QY 241 GCACGAGCCGCTACGGGAGGCGGACCTTCAATTAAGACCGCCTTCCCGGGGGCGAG 300
 DB 241 GCACGAGCCGCTACGGGAGGCGGACCTTCAATTAAGACCGCCTTCCCGGGGGCGAG 300
 QY 301 ACCGGTTTGAAGTGTGGCGCTTGTATGCGCACTGCGAAGGTGACGCTCCCAAGGCGT 360
 DB 301 ACCGGTTTGAAGTGTGGCGCTTGTATGCGCACTGCGAAGGTGACGCTCCCAAGGCGT 360
 QY 361 TTCTGCTGAAGTCCAGGCTCGAGGAGAGTGGGATAGGGAATCCAAATTTGGATTGGGTTATG 420
 DB 361 TTCTGCTGAAGTCCAGGCTCGAGGAGAGTGGGATAGGGAATCCAAATTTGGATTGGGTTATG 420
 QY 421 TCGGTGTGCGATGACGAGACGAGTGGGTGGCGGAGCAAGGGAAGGTGTATGTGGTGT 480
 DB 421 TCGGTGTGCGATGACGAGACGAGTGGGTGGCGGAGCAAGGGAAGGTGTATGTGGTGT 480
 QY 481 GGAGAGGAGCTTGTAGGGATTATGAGTGGGTTGATGTTCTTGTGCTCACTTGAAGTCTG 540
 DB 481 GGAGAGGAGCTTGTAGGGATTATGAGTGGGTTGATGTTCTTGTGCTCACTTGAAGTCTG 540
 QY 541 CTCACTCTTTTGTTCGCACTCAACAACTACTCATGTTGAAAAGGTGAAAATAGAGAA 600
 DB 541 CTCACTCTTTTGTTCGCACTCAACAACTACTCATGTTGAAAAGGTGAAAATAGAGAA 600
 QY 601 AGAAGAGCATTCATTAATCAAGTTGGTACGACTGTTTCAATATCAACCTAAGTTCG 660
 DB 601 AGAAGAGCATTCATTAATCAAGTTGGTACGACTGTTTCAATATCAACCTAAGTTCG 660
 QY 661 CGTCCAAAGACAAAGAAAGAAAGGAGCGACGACGAGATGATGACGACCCCAAGTATG 720
 DB 661 CGTCCAAAGACAAAGAAAGAAAGGAGCGACGACGAGATGATGACGACCCCAAGTATG 720
 QY 721 AAGGTGGATGACATATATACATTCGGAGGATCCCAATTCACCTTCACAAAATCTAATG 780
 DB 721 AAGGTGGATGACATATATACATTCGGAGGATCCCAATTCACCTTCACAAAATCTAATG 780
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 DEFINITION
 DNA coding for plant lipase, transgenic plant and method for
 controlling senescence of plant.
 ACCESSION
 BD268753
 VERSION
 BD268753.1
 KEYWORDS
 JP 2002536979-A/1.
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 ORGANISM
 DIANTHUS CARYOPHYLLUS
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 Caryophyllales; Caryophyllaceae; Dianthus.
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 Thompson,J.E., Wang,T.W., Hudak,K. and Hong,Y.
 DNA coding for plant lipase, transgenic plant and method for
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 Patent: JP 2002536979-A 1 05-NOV-2002;
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 DEFINITION
 ACCESSION
 VERSION
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 SOURCE
 ORGANISM
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 1 (bases 1 to 1341)
 Hong, Y., Wang, T.W., Hudak, K.A., Schade, F., Froese, C.D. and
 Thompson, J.E.
 An ethylene-induced cDNA encoding a lipase expressed at the onset
 of senescence
 Proc. Natl. Acad. Sci. U.S.A. 97 (15), 8717-8722 (2000)
 10890894
 2 (bases 1 to 1341)
 Hong, Y., Hudak, K.A. and Thompson, J.E.
 A cDNA clone from Dianthus caryophyllus encoding a
 lipid-protein-particle associated lipase
 Unpublished
 3 (bases 1 to 1341)
 Hong, Y., Hudak, K.A. and Thompson, J.E.
 Direct Submission
 Submitted (23-SEP-1997) Biology, University of Waterloo, 200
 University Ave. W., Waterloo, Ont. N2L 3G1, Canada
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1 Harper, J.F., Kreps, J., Wang, X. and Zhu, T.				
Stress-regulated genes of plants, transgenic plants containing				
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RESULT 5
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ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AY079356	GI:19310712	FLI CDNA	Arabidopsis thaliana (thale cress)	Arabidopsis thaliana	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Etgu, P., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.	Arabidopsis Open Reading Frame (ORF) Clones	Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA	The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPF CDNAs (RAPF CDNA: 'RIKEN Arabidopsis Full-length cDNA') (Seki, M., Narusaka, M., Ishida, J., Hayashizaki, Y. and Shinozaki, K.					
The Salk, Stanford, PSEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAPF CDNAs: Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.													
Yamada, K. (SSP/PSEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PSEC) contributed equally to this work as PIs.													
Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.													
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 Best Local Similarity 57.9%; Pred. No. 4,6e-62;
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 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

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 1 (bases 1 to 1348)

REFERENCE
 AUTHORS
 Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
 Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
 Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
 Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
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 Davis,R.W., Ecker,J.R. and Theologis,A.
 Arabidopsis Full Length cDNA Clones

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

Unpublished
 2 (bases 1 to 1348)
 Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Banno,F., Dale,J.M.,
 Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L.,
 Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L.,
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 Southwick,A., Tracy,S.E., Shinzaki,K., Davis,R.W., Ecker,J.R. and
 Theologis,A.
 Direct Submission
 Submitted (07-AUG-2001) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN
 Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinzaki,K.

COMMENT
 The Salk, Stanford, PGSC (SSP) Consortium members carried out the
 sequencing and annotation of the RAPL cDNAs: Yamada,K., Liu,S.X.,
 Pham,P.K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D.,
 Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,
 Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H.,

Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shim, P., Southwick, A., Tracy, S.E., Davis, R.M., Becker, J.R. and Theologis, A., Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

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Best Local Similarity 57.9%; Pred. No. 4.7e-62;
Matches 752; Conservative 0; Mismatches 466; Indels 81; Gaps 4;

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controlling senescence of plant.
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BD268758
VERSION
BD268758.1 GI:33078526
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JP 2002516979-A/6.
SOURCE
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ORGANISM
Arabidopsis sp.

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1 (bases 1 to 1167)

Thompson, J.E., Wang, T.W., Hudak, K. and Hong, Y.
DNA coding for plant lipase, transgenic plant and method for controlling senescence of plant

JOURNAL

Patent: JP 2002536979-A 6 05-NOV-2002;

COMMENT

SENESCO INC

OS Arabidopsis sp.

PN JP 2002536979-A/6

PD 05-NOV-2002 JP 2000599888

PF 14-FEB-2000 JP 2000599888

PI 16-FEB-1999 US 09/250280

PR JOHN E THOMPSON, TZANN WEI WANG, KATALIN HUDAK, YUWEN HONG PC

C12N15/09, A01H5/00, C12N1/21, C12N5/10, C12N5/20, C12N15/00, C12N5/ PC

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CC DNA coding for plant lipase, transgenic plant and method for

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FT Key Location/Qualifiers

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LOCUS

DEFINITION Sequence 15 from patent US 6774284.

ACCESSION AR576378

VERSION AR576378.1 GI:56578433

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

Senesco, Inc.; New Brunswick, NJ

Location/Qualifiers

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ORIGIN

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Best Local Similarity 64.3%; Pred. No. 1.3e-49;

Matches 453; Conservative 0; Mismatches 248; Indels 3; Gaps 1;

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REFERENCE
 AUTHORS Lin, X., Kaul, S., Shea, T.P., Fujii, C.Y., Shen, M., Vanaken, S.E., Barnstead, M.E., Mason, T.M., Bowman, C.L., Rensing, C.M., Benito, M.-I., Carrera, A.J., Creasy, T.H., Bell, C.R., Town, C.D., Nierman, W.C., Fraser, C.M. and Venter, J.C.
 Unpublished
 2 (bases 1 to 96685)
 Lin, X.

JOURNAL
 TITLE Direct Submission
 AUTHORS Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
 REFERENCE 3 (bases 1 to 96685)
 Town, C.D. and Kaul, S.
 TITLE Direct Submission
 JOURNAL Submitted (27-FEB-2002) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA, cdtown@igf.org
 On Apr 18, 2002 this sequence version replaced gi:6598662.
 On Mar 7, 1999 this sequence version replaced gi:161616.
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COMMENT
 The annotation of this entry was produced with considerable contributions from Stephane Rombauts and Pierre Rouze, Department of Genetics, University of Ghent, Ledeganckstraat 35, 9000 Ghent, BE, E-mail: strom@genengp.rug.ac.be, piro@genengp.rug.ac.be A more detailed annotation of this entry and other sequences from the long arm of chromosome 4 can be viewed at: <http://webavr.mips.biochem.mpg.de/proj/thal/> this fragment has an overlap with ATAN22 at the 3 end.

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DEFINITION      Arabidopsis thaliana chromosome 2 clone F7D19 map m51, complete
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ORGANISM      Arabidopsis thaliana
REFERENCE      1. Lin, X., Kaul, S., Shea, T. P., Fujii, C. Y., Shen, M., Vanaken, S. B.,
AUTHORS      Barnes, M. E., Mason, T. M., Bowman, C. L., Romling, C. M.,
Benito, M., I., Carrera, A. J., Creasy, T. H., Buell, C. R., Town, C. D.,
Niernan, W. C., Fraser, C. M. and Venter, J. C.
Unpublished
2. (bases 1 to 115310)
3. (bases 1 to 115310)
JOURNAL      Lin, X.
REFERENCE      Direct Submission
AUTHORS      Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
JOURNAL      Medical Center Dr., Rockville, MD 20850, USA
REFERENCE      3. (bases 1 to 115310)
AUTHORS      Town, C.D. and Kaul, S.
JOURNAL      Direct Submission
REFERENCE      Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
AUTHORS      Medical Center Dr., Rockville, MD 20850, USA, cdtown@igr.org
COMMENT      On Apr 18, 2002 this sequence version replaced gi.16598641.
On Oct 8, 1997 this sequence version replaced gi.2443866.
We have determined that YAC YUP812 is chimeric, and is comprised
of two distinct genomic EcoRI fragments from chromosome I. This
submission contains the sequence from the EcoRI site at position 1
(right end) to position 181918 of our previous Phase II
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OY	269	AATTATTAAGACCGCTCTCCGGGGGGGACACCGGTTTACGAGTGACGGTCCGTAATTGTA	328
Dd	104258	CTTCGACAAAG--GTCAATGCTCGAAAACGCTTCCATACGAGGTGTAACTTCTCTA	104314
OY	329	CGCCACTGCAAGAGTCAGAGCTCCAGAGCGCTTTGTGCTGAAGTCGAGGTCGAGGAGAA	388
Dd	104315	CGCCACAGCTCGTGTCTCTCTCCCGAAGTTTGCTTCCAAATCACAATCAAGAGATTTC	104374
OY	389	GTCGATAGGGAATGAATTTGATTTGGGATGTCTGTGTGCAATGACGAGACGAGTGC	448
Dd	104375	TTCGGAACGTGAGCTTAACTGGTTTTGGGCTACATTCCTGTCAGTGTGATGAACGCTCTAA	104434
OY	449	GTCGCGGAGACGAAGGAGGCTAATGTGTGTGAGAGGACATTGTAAGGATTAATAGTG	508
Dd	104435	GACTTTAAGACGCGCTGAGATCTAATATGCTTTGAGAGGAAGAGAGGAACATATAGATG	104494
OY	509	GATTGATGTTCTTGTTGTCAACTTGAGTCTGCTCATCTTTGTTACGCACTCAACAAAC	568
Dd	104455	GCTCATGTTTGGGTGTCTAGGCCAACTTCAGCTGACCCCTTGCTGACGAGCCGAGCA	104554
OY	569	TACTGATGTTGAAAAGGTGAAAAATAGAGAAAAAGACATTCATAAATCAAGTTGGTA	628
Dd	104555	GGATGCTTCTGGTGTGTAGTTGA--	104583
OY	629	GGATGCTTCAATATCAACTTACTAGGTTCCGCTCCAAAGCAAAAGAAAAAGAACCA	688
Dd	104584	GGAATTT-----GATGTGA	104599
OY	689	CGAGCAGATGATGACGACCCCAAGTGTGCAAGGTTGATGACAAATTATACATCCGA	748
Dd	104600	CAGTGAATGAGGAAGGGGTGTAGAGTGTCTCGGGTGTCTACAAATCTAATCTTCTAA	104655
OY	749	GGATCCCAATACCCCTTACAAAATTAAGTGCAAGAACACAACTTCAGACCAACTCAA	808
Dd	104660	TCACCCGAAATCGAATTCATCTAACCTGATGAGGTCAAGGTCAAGTTGTTAGCCAAATCAA	104719
OY	809	ACAATTAATGACAAAATACAAAGACGAACCTTAAGCATACATTGCGCGTCAACGCT	868
Dd	104720	GGAGCTTCTGTTAAGTAAAGTAAAGACGAAACCGAGCAATTGTGTGACATGCAATGTCT	104779
OY	869	AGGCGCGACATATAGTCGTGAGGCGCTTGACATPATGAGGAGAA---TCTACGACCGA	925
Dd	104780	GGAGACTVACAGAGGCTGTCTGGCGCCCTATATATATAGCTGAGAACGGTTTCCATGTATGA	104839
OY	926	GATCCCAATACGCGCGTGTCTTCCGGGTCCCAAAAGTACGCAACAAAATTTCCACA	985
Dd	104840	TGTTCCGATCATCTGTATAGTCTTGTGTGTGTCACAGTATGAAACAAAGAGTTACAGA	104899
OY	986	ACTCTTGACCTGTACCCAAACCTAATATGTCTCATATGAGAAATGTATGACTGAT	1045

Db 104900 CGAAGTAATGATGCAAGAACTTAAAGATCCTCATGTAGTAAGAACAGATTGCTCTT 104959
 Qy 1046 CCTCTGTATCCCTGAACTCATAGGTTAGTGAACATAGGAATTCAGCTGGAGATCGA 1105
 Db 104960 AACTCGATACCGAGGGGACTTTAGGGTATGTGACATAGGAATTAACCTTTGTGATCGA 105019
 Qy 1106 CTGAGAGAGTGCAGCTTTCTTAAAGAACTCGAAAAACCCGAGTATGGCATTAATTT---- 1161
 Db 105020 TACAAAGAGTCACTCTTCTTAAGCATTTCAAGGAATTCAGGGATTTGGCATTAATCTTCA 105079
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 Db 105080 GGTAAAGATCTGTGAGAAATCTTTCAATTGACTCAACAGATACAGATAGAAAATT 105139
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 Db 105140 TTACATATTTTTCATGTATGTGTGCGAGGAGATTCATGTGTAGCTGATGGAATG 105199
 Qy 1198 GGGTTAAGGGGAGTTTAAAGGTTGTAATAAGAGAGTTCATTTGTTAATAGTCAAT 1257
 Db 105200 GGAAGAAAGAGAGTTTAACTGATGTAAAGAGAGATTCATTAAGTGAACAGTCAAT 105259
 Qy 1258 GTGATTTTCTTAAGAGAAATGTTGTTCTCTCAGCTTGGTGGGTTGTGAGAACAAAG 1317
 Db 105260 GCGAGTTCTTGAAGCTGAGTGTGTGGTCCAGGATCTTGGTGGGTAGAGAAACAAAG 105319
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 Db 105320 GACTGATCAAGAGAGAGATGTGATGGGTTCTTGTCTCCGTTGAGAGAGAACCTGTAC 105379
 Qy 1378 CTGAATT 1384
 Db 105380 CTGAATT 105386
 RESULT 11
 BT009343 1639 bp mRNA linear PLN 20-JUN-2003
 LOCUS Triticum aestivum clone wlm4.pk0021.h10.f16, full insert mRNA
 DEFINITION
 ACCESSION BT009343
 VERSION BT009343.1 GI:32128894
 KEYWORDS FLI CDNA.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 1639)
 Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
 Direct Submission
 Submitted (20-JUN-2003) Crop Genetics, E. I. Dupont de Nemours and
 Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
 USA
 FEATURES
 source Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wlm4.pk0021.h10.f16"
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 Best Local Similarity 56.9%; Pred.No.1.3e-26;
 Matches 399; Conservative 0; Mismatches 283; Indels 19; Gaps 3;
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 Qy 747 GAGATCCCAATGACCTTCACAAAATAAGTGCAAGACAACTTCAACCAACTC 806

Db 643 ACCGACGAGCGTCCCTCTTCTCCAGTACAGCCGACGACAGCTGTGGCCACGCT- 701
 Qy 807 AAAAATTAATGACAAAATTAAGAGAAACCTTAAGCATTAACATTCGCGGTCAGAC 866
 Db 702 GGGAACTGTGTGCAAGTAAAGAGGAGAGGCTCAGCATCTCTGTGACCGGGACAGC 761
 Qy 867 CTAGCCGCGACACTATGATGTGTAGCGCTTCGACATAGTGAATAATTCACACGCGAG 926
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 Db 942 AAGCCCACTCATCTCCGCTCTACCGACGACCTCTCGCTACGCAACGTGGGAC 1001
 Qy 1092 GAGCTGAGATGCACTCGAGAGTCACTTTCTAAA--GACTGAAAAACCCGAGT 1148
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 Qy 1149 GATTGCAATATTGCAAGCAATTTGCATGTTTAAGTGTGTGGCATGGGTTAAAGGG 1208
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 LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:J013055J12, full
 DEFINITION
 ACCESSION AK098952
 VERSION AK098952.1 GI:32984161
 KEYWORDS Oryza sativa (japonica cultivar-group)
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1
 The Rice Full-length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-length cDNA Project Team,
 Kikuchi,S., Sato,K., Nagata,T., Kawagashira,N., Doi,K.,
 Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
 Kojima,K., Namiki,T., Ohneda,E., Yabagi,W., Suzuki,K., Li,C.,
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 Kurossaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
 Nakikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nishikura,Y.,
 Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
 Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN,
 Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arahawa,T., Fukuda,S.,
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Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
Japanese rice
Science 301 (5631), 376-379 (2003)

2 (bases 1 to 1805)
12869764

JOURNAL
PUBMED
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Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
Nami, T., Narikawa, R., Nishikawa, R., Nishikawa, T., Nomura, K.,
Nunasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H.,
Ose, N., Ota, Y., Otsu, Y., Ryu, R., Satoh, H., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
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Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W.,
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305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp.
Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28k full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-Length_cDNA_Project_Team_Kikuchi_S.,Satoh_K.,Nagata_T.,Kawagashira_N.,Doi_K.,Kishimoto_N.,Yazaki_J.,Ishikawa_M.,Yamada_H.,Ooka_H.,Hotra_I.,Kojima_K.,Nami_K.,Ohneda_E.,Yahagi_W.,Suzuki_K.,Li_C.,Ohtsuki_K.,Shishiki_T. and Yamamoto,M.

FAS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
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Kodama, T., Kurosaki, T., Kusneger, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Nishikawa, R., Nishikawa, T., Nomura, K.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
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Hiroaka, T., Hotra, I., Iida, J., Imamura, K., Imochi, K., Ishii, Y.,
Ishikawa, T., Itoh, F., Iida, J., Imamura, K., Imochi, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunasaki, R., Ohno, M., Ose, N.,
Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
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Yasunishi, A. and Hayashizaki, Y.

Location/Qualifiers
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/mol_type="mRNA"
/culti_type="Nippobare"
/db_xref="taxon:39947"
/clone="J013055J12"

ORIGIN

Query Match 10.9%; Score 167.2; DB 15; Length 1805;
Best Local Similarity 54.6%; Pred. No. 6.4e-24;
Matches 368; Conservative 0; Mismatches 288; Indels 18; Gaps 1;

Qy 714 GTGATCGAAGTGGATGATGACATATATACATCGGAGATCCAAATGACCTTCACAAA 773
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Qy 774 CTAAAGTCGAAGACACACTTTCAGACCAAACTCAAACACTTAATGACAAAATACAAAG 833
Db 714 TACAGCCCGCGCGACGACGATGCTCGCACCGTGGCGACAGCTGGTGGAGATACGAAAC 773
Qy 834 GAAACCTTAAGCATTAATTCGCGGTGACAGAGCTAGCGGACACTATCATAGTGTGAGC 893
Db 774 GAGAGCTCGCGCTGCTGTGACGAGGACAGAGCTCGAGCGCTGCTGCGCACGCTTGC 833
Qy 894 GCGTTGACATAGTGGAGAAATCTCACACCGAG-----ATCCAGTC 935
Db 834 GCGTTGATATTCGTCGTCGTCGACGAGGTGCCAAGGTGCGCGACGCGGACATCCGCTG 893
Qy 936 AGCGCGCTGCTTTCGGGTGCGGACCAAAAGTGGCAACAAAATTCACCAACTTTGAC 995
Db 894 ACCGCGTGGTTCGGGAGCGCGACATCGGGAACCGGAGTTCAAGAACAGTTGAG 953
Qy 996 TCGTACCCAAACCTAAATGTCCTCATGTAAAGATGTCATCGACCTGATCCCTGTAT 1055
Db 954 GAGCAGCCCAACCTGCGGCGCTGCAGTACGAGAACATGCCGACCTCATCCGCTTAC 1013
Qy 1056 CCCGTGAACCTCATGGGTACGTGACATAGATCGAGTGGAGATCGACTCGAGAG 1115
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Qy 1236 GTTCATGTTGTAATTAATGATGATGATTTCTTAAGAGAAATGTTGTTCTCCAGCT 1295
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Qy 1296 TGTGGTGTGTCGAACCAAGGATGTTTGAATTAAGATGATGAGTGGCTTGGCT 1355
Db 1254 TGTGGTGTGAGAGAAACCAAGCATGTGCTCGGACGAACGGGAGATGGCAGCTGAG 1313
Qy 1356 CTTCTGAGGAAGA 1369
Db 1314 GGGCCCGCAGAGA 1327

RESULT 13
AK104373
LOCUS 1810 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:001-035-F02, full
insert sequence.
ACCESSION AK104373
VERSION AK104373.1 GI:32989582
KEYWORDS FULL_CDNA; oligo capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
1
The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team:
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotra, I.,
Kishikawa, M., Nami, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Otsu, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,

Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikawa, J., Ikeda, R., Iehibiki, J., Kawamata, M., Yoshimura, A., Mura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Hayatsu, N., Imocani, K., Ishii, Y., Itoh, M., Kigawa, I., Kondo, S., Konno, H., Miyazaki, A., Oato, N., Oca, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from *Japonica* rice
Science 301 (5631), 376-379 (2003)
12869764

2 (bases 1 to 1810)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashizaki, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, P., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imocani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kigawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Maeda, H., Matsubara, K., Matsuyama, T., Mura, J., Nakamura, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nishikawa, J., Nishi, K., Nomura, K., Numaaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Oato, N., Oca, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., and Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, U., Yokomizo, S., and Yoshimura, A.

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Tel:81-29-838-7007, Fax:81-29-838-7007
This clone is one of the 28K full-length cDNA clones from *Japonica* rice.
URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

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FLS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Iehibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Maeda, H., Mura, J., Mizuno, K., Narikawa, R., Nishikawa, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.

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Location/Qualifiers
1. 1810
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Best Local Similarity 54.5%; Pred. No. 1,4e-23;
Matches 367; Conservative 0; Mismatches 289; Indels 18; Gaps 1;
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RESULT 14
AKI06129
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) cDNA clone:001-207-F09, full insert sequence.
AKI06129
ACCESSION
AKI06129.1 GI:32991338
VERSION
FLI CDS; oligo capping.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1
REFERENCE
The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team.

ORGANISM

Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS

The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team:
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C.,
Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otono, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Teunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niihara, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusunegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imocani, K., Ishii, Y., Itoh, M.,
Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Oato, N., Oka, Y.,
Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
12869764
2 (bases 1 to 1921)

TITLE

JOURNAL

PUBMED

REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hirotsu, K., Hirooka, T.,
Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K.,
Imocani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Kurosaki, T., Kusunegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,
Namiki, T., Narikawa, R., Niihara, J., Nishi, K., Nomura, K.,
Numasaki, R., Ohneda, E., Otono, M., Ohtsuki, K., Oka, M., Ooka, H.,
Oato, N., Oca, Y., Otono, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and
Yoshimura, A.

TITLE
JOURNAL

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)

COMMENT

This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., and
Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Otono, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusunegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Niihara, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Teunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hirotsu, K.,
Hirooka, T., Hori, F., Iida, J., Imamura, K., Imocani, K., Ishii, Y.,

FEATURES
SOURCE

Location/Qualifiers
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ORIGIN

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Best Local Similarity 54.5%; Pred. No. 1,4e-23;
Matches 367; Conservative 0; Mismatches 289; Indels 18; Gaps 1;

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Qy 774 CTAAAGTCAGAACACACATTCAGACCAAACTCAAATATGACAAATTCAAAGAC 833
Db 715 TACAGCGCCCGACACACAGATCTCGCCGCTGCGAGCTGTGGAGATACAGAAC 774
Qy 834 GAAACCTTAAGCATTAACATTCGCGGTGACAGCTAGCGCCGACATCATGATGATGAC 893
Db 775 GAGAGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 834
Qy 894 GCTTTCACATTAAGTGAAGAAATCTACGACCGAG-----ATCCAGTC 935
Db 835 GCGTTGATATCTGTCGTCACAGCGGTGTCACAGGTGCGCGACGCGACATCCGCTG 894
Qy 936 ACGCGCTGCTCTTGGGTGCTCCCAAAAGTAGCAACAAATTCACAACTCTTGAC 995
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Qy 1356 CTTCTGAGAGAGA 1369
Db 1315 GGGCTCGCAGAGGA 1328

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2005, 07:12:03 / Search time 6638.82 Seconds
(without alignments)
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Perfect score: 1537
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: gb_gaet3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	290	18.9	688	6	CN604658 USDA_FP_1
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6	275.4	17.9	593	2	BG321342 Dn01_07e0
7	272.4	17.7	684	2	BE474050 sp58e01.Y
8	271	17.6	707	6	CA839368 MCT02605
9	265.4	17.3	698	1	CD397937
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11	253.4	16.5	648	1	BX835390 BX835390
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14	228.6	14.9	696	5	CV708865 UCRPT01_0
15	227	14.8	697	5	BQ989600 QGF18B22
16	225.4	14.7	592	6	BQ989130 QGF16N11
17	223	14.5	764	7	CB288473 V-B-15D07
18	221.4	14.4	621	8	CV710652 UCRPT01_0
19	220.4	14.3	625	7	CX517885 st3dnP2dD
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30	206.6	13.4	722	8	CX714579
31	204.8	13.3	639	7	CN181511
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
Arabidopsis thaliana Full-length cDNA Complete sequence from clone GS1951592D2 of Siliques of strain col-0 of Arabidopsis thaliana (thale cress).

ACCESSION
BX821625
VERSION
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)

REFERENCE
AUTHORS
TITLE
A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction; Temple G.
Genoscope members carried out sequencing and annotation; Castellani V., Aury J.M., Jailion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
USGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length
http://www.genoscope.cns.fr/cgi-bin/gdb/gdb?source=Arabidopsis.

FEATURES
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Best Local Similarity 57.6%; Pred. No. 2.8e-67;
Matches 749; Conservative 0; Mismatches 468; Indels 83; Gaps 6;

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Db 1151  TGCCAGATCTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1210
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RESULT 2
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LOCUS
DEFINITION
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CN604658
VERSION
KEYWORDS
ACCESSION
CN604658
DESCRIPTION
EST.
SOURCE
Vitis shuttleworthii
Vitis shuttleworthii
ORANISM
Eukaryote; Vitidipantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosidae; Vitaceae; Vitis.
1 (bases 1 to 661)
REFERENCE
Hunters, W., Dang, P., Chaparro, J., Lu, J. and Leong, S.
Expressed Genes in Vitis shuttleworthii L
Unpublished (2004)
JOURNAL
COMMENT
Contact: Wayne Hunter, Phat Dang, USDA, ARS; Jiang Lu, FAMU
U.S. Horticultural Research Lab
USDA-ARS; FAMU
Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898; (850) 412-7393
Fax: (772) 462-5986; (850) 561-2617
Email: whunter@uhr1.ars.usda.gov, pdang@uhr1.ars.usda.gov,
jiang.lu@famuc.edu
Seq primer: T3 Primer.

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FEATURES

source

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by PM Dang, USDA, ARS, U.S. Horticultural Research Lab,
Ft. Pierce, FL, USA."

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ORIGIN

Query Match 19.2%; Score 295; DB 7; Length 661;
 Best Local Similarity 66.6%; Pred. No. 5e-60;
 Matches 440; Conservative 0; Mismatches 215; Indels 6; Gaps 1;

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QY 775 TAAGTCAAGACACCACTTCAGACCAACCAACCACTAATGACAAATACAAAGC 834
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QY 835 AAACCCCTAAGCATTAACATTCGCGGTCAAGCCTAGCGGACACTATCACTCGTGAAG 894
 DB 121 AGAAGATGACATCATGTGACAGGTCAAGCCTGGGTGAGGTCTAGCAGTATGAGCT 180

QY 895 CTTTCGACATAGT-----GAGAAATCTACGACCGAGATCCAGTCAAGGCGGTGCT 948
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QY 1009 TAAATGCTCTCAATGTAAGGATGTCACTGACCTGATCCCTGTATCCGCTGAACCTCA 1068
 DB 301 TCCACATCTCTCAATGTAAGGATGTCACTGACCTGATCCGCTGTATCCGCTGAACCTCA 360

QY 1069 TGGGTTACGTGAACATAGAAATGAGTGAAGATGACTGAGGAAATGCACTTTCTAA 1128
 DB 361 TCGGCTATGTGAAGACGGAACCTGAGCTAGCTAGCTAGGAAATGCTCCAACTTGA 420

QY 1129 AGGACTCGAAAAACCCAGTATGTCGATATTTGCAAGCAATTTGCAATGTTAAGT 1188
 DB 421 AGGATTCGAAGAACCCGCTGACCTGCAAACTTGCGAGGATGTGATGTGCTG 480

QY 1189 GTTGGCATGGGGTTAAGGGAGTTTAAAGTTGTAATTAAGAAAGTTGTCATTGTTA 1248
 DB 481 GTTGGATGGGGCCAAATGCAAGTTTGAATCTCAAGTGAAGAGAGCTTGCCCTTGGTGA 540

QY 1249 ATAAGTCATGTATTTCTTAAGGAGAAATGTTGTTCTCCAGCTTGGTGGTGTGC 1308
 DB 541 ACAAGTCTCTTAATTTCTCAAGGATGATGCTGTTCCAGCGTCAAGGTGGGTGAGA 600

QY 1309 AGAACAAGGAGATGTTTGAATTAAGATGATGAGGTGTTGGTCTCTCTTAAGAG 1368
 DB 601 AGAACAAGGAGATGATGAGAAACAGATGAGATGAGGTGAGCAAAATCAACCCGAG 660

QY 1369 A.1369
 DB 661 A.661

RESULT 3
 CD860766/c 688 bp mRNA linear EST 11-JUL-2003
 LOCUS TNE.002N24F011204 TNE Pisum sativum cDNA clone TNE002N24, mRNA
 DEFINITION
 ACCESSION CD860766
 VERSION CD860766.1 GI:32544582
 KEYWORDS EST.
 SOURCE Pisum sativum (pea)
 ORGANISM Pisum sativum
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosoids; eurosoids I; Fabales; Fabaceae; Papilionoideae; Viciales;
 Pisum.
 REFERENCE 1 (bases 1 to 688)
 AUTHORS Genopiante.
 TITLE Genopiante, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genopiante
 Genopiante

93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genopiante' (<http://www.genopiante.com>
 and <http://genopiante-info.infodigen.fr>).
 Location/Qualifiers
 1..688
 source
 /organism="Pisum sativum"
 /mol_type="mRNA"
 /cultiivar="Terese"
 /db_xref="taxon:3888"
 /clone="TNE002N24"
 /rissue_type="scipule"
 /clone_lib="TNE"

ORIGIN

Query Match 18.3%; Score 290; DB 6; Length 688;
 Best Local Similarity 65.2%; Pred. No. 8.1e-59;
 Matches 442; Conservative 0; Mismatches 235; Indels 1; Gaps 1;

QY 688 ACAGACGATGATGACGACCCCAAGTATGACAGGTTGATGACAAATATACATCGG 747
 DB 687 ATGAGATGACCAAGGCTGCCAAGATATGAAAGGTTGGCTGACCATATACCTCAG 628

QY 748 AGGATCCCAATCACCTTCACAAACTAAGTCAAGACACAACTTCAGACCAACTCA 807
 DB 627 ACAGCCCAATATCTCTTTCATCAAAACAGCGTGAATCCAGATTCCTAACAAGATTA 568

QY 808 AACAACTAATGACAAATATACAAAGCAAAACCTTAAGCATTAATTCGCGGTACAGCC 867
 DB 567 AAAGTTGTTGAACATTTACAGAAATGAATCCAGTGTGTATTTGTTGGTGGACACATGC 508

QY 868 TAGCGGACACTATCATGTGTGAGCGCTTCGACATAGTGAATCTCAGACGAGAG 927
 DB 507 TAGGAGC-AGTCTATCACTGTGTGATGCTTTGATTTGTGCAAGATGATGTAACAGCA 449

QY 928 TCCAGTCAAGCGCGGTGCTTCGCGGTGCCCAAAAGTAGGCAACAAATTCCAACAC 987
 DB 448 TTCCCGTGAAGCTTTGTGTGTTGGTTCCTCCACAAAGTGGGAACAAAGATTCATGATCA 389

QY 988 TCTTCGACTGTACCCCAACCTAATGTCCTCATGTAAAGATGTGATGACTGATTC 1047
 DB 388 GGTTCAAAAGTTTCCGAATTTGAAGGTGTTACACGTGAAGAAATGTGATGATCTTATAC 329

QY 1048 CTCTGTATCCCGTGAACCTATGAGGTGATGCTGAACATAGGAATGACTGAGATGACT 1107
 DB 328 CGCATTAATCCAGGAAAGTTATTTGGGGTATAGATATACAGGTGTAGAGTTGGTGAATTA 269

QY 1108 CGAAGAGTGCACCTTCTAAGGACTCGAAAAACCCGAGTGAATTCATTAATTTGCAAG 1167
 DB 268 CAGGAAATCAACGAGTTTGAATGATGATTCGAAGAAATCCGAGTGAATTTGCAAG 209

QY 1168 CAATATTCATGTTGTAAGTGTGTCATGAGGTGAAGGGGAGTTTAAGGTTGTAATA 1227
 DB 208 CTATGTTGATGATGATGCTGCTGTTGGAATGGAAGTGAAGGAGTTGAAGTTGAAGGTGA 149

QY 1228 AGAAGATGTTGATGCTGTTGTAATTAAGTCAATGATTTTCTTAAGGAAGATGTTGGTTC 1287
 DB 148 AGAAGATGTTGCTTTGTTGTAATTAAGTCTGTGATTACTTAAGGAAGAGTGCATGTGC 89

QY 1288 CTCAGCTTGTGGGTGTGACAGAAACAAAGGAGATTTTGAATTAAGATGATGATGGG 1347
 DB 88 CAGGTCATGATGATGATGAGAAAGATTAAGGTTTGTGTAAGAGGAAAGATGAGAAATGG 29

QY 1348 TTTTGGCTCTCTCTGAGG 1365
 DB 28 TTGATGATCCTGCCGGG 11

RESULT 4
 AM132739/c 621 bp mRNA linear EST 08-JUL-2004
 LOCUS AM132739

	DEFINITION	seq9e10.y1 Gm-cl013 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl013-3043 5' similar to TR:Q9ZTW1 Q9ZTW1 LIPASE ;, mRNA Sequence.					
	ACCESSION	AW132739					
	VERSION	AW132739.1 GI:6134346					
	KEYWORDS	EST.					
	SOURCE	Glycine max (soybean)					
	ORGANISM	Glycine max					
	REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.					
	AUTHORS	1 (bases 1 to 621) Shoemaker R., Keim P., Vodkin L., Erpelting J., Coryell V., Khanna A., Bolla B., Marra M., Hillier L., Kueba T., Martin J., Beck C., Wylie T., Underwood K., Steptoe M., Theising B., Allen M., Bowers Y., Person B., Swaller T., Gibbons M., Page D., Harvey N., Schurk R., Ritter E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann R., Waterston R. and Wilson R.					
	TITLE	Public Soybean EST Project					
	JOURNAL	Unpublished (1999)					
	COMMENT	Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. Possible reversed clone: similarity on wrong strand This clone is available through: Biogenetic Services, 801 32nd Ave, Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Seq primer: -40RP from Gibco High quality sequence scop: 407. location/Qualifiers 1..621 /organism="Glycine max" /mol_type="mRNA" /cultivar="Williams" /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Gm-cl013-3043" /tissue_type="whole seedlings, 2-3 week old seedlings, greenhouse grown" /lab_host="XLR0-Gold" /clone_1lb="Gm-cl013" /note="Vector: pBluescript II XR; Site 1: EcoRI, Site 2: XhoI. This cDNA library was constructed from mRNA isolated from whole seedlings of 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragment were transformed into XLR0-gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelting."					
	FEATURES						
	source						
	ORIGIN	18.5%; Score 283.6; DB 1, Length 621; Best Local Similarity 66.6%; Pred. No. 2.8e-57; Matches 403, Conservative 0, Mismatches 202, Indels 0, Gaps 0,					
QY		783 AGAACAACAATTGCAGCAAACTCAATGAACAAAATCAAGAAGCAAACTTCA 842					
DB		621 AGAGCGCAGTTTCAGGCCACGTCAAATCCCTTTACACCATTACAGCTTTAGACCCA 562					
QY		843 AGCATTAACATTGGCCGCTACAGCGCTGAGGCGAGACTATCACTGCTAGCGCCCTTGAC 902					
DB		561 GCCCTTGTCATGCTGGGGCAGACGCTCGCGCGCAACCTATTCATGCTGAGCGCCCTTGAC 502					

QY	903	ATAGTGGAGATCTCACAGCCGAGATCCCACTCCAGCCGCGTGTCTTCGGGTGCCAAAA	962
Db	501	CTGTGTCAAAAACGGGGTAAACGMAGTCCCGGTCAACGCATCGTGTCCGCTCCCCAG	442
QY	963	GTAGCAACAACAAAAATTCACAACTCTTCGACTCGTACCACCACTAAATGTCCCTCAT	1022
Db	441	GTCCGAAACAAAGCCCTTCACGAGAGGTTCAACATGTTCCGAACCTTGAAAGTTTGAC	382
QY	1023	GTAAAGATGTCATCGACCTGATCCCTCTGTATCCGTAAACTCATGGTTACGTGAAC	1082
Db	381	GTAAAGAACGTGATCGATTTGATCCCACTACCCGGGGAAGTTGTAAGGTATGAGTAC	322
QY	1083	ATAGGAATCGAGCTGAGATCGACTCGAGGAATCGACTTTCTAAAGGATCGAAAAAC	1142
Db	321	ATGGGCACGAGCTGTGATAGACACGAGGAAGTCGCGAGCTTGAAGGATCTCAGGAAC	262
QY	1143	CCGAGTATTTGGCTAATTTGCCAGCAATTTGATGTTGTAAGTGGTCATGGGGTT	1202
Db	261	CCGGGTATTTGGCTAATCTTGCAAGCAATGTTGATGTGTGGCGGGGTGAAATGGGAAG	202
QY	1203	AAGGGGAGTTTAAAGTTGTAAATPAAGAGAGTGTGCATGTTTAAATPAATCATGTGAT	1262
Db	201	AAGAGAGATTTGAGATGAGGAGTAAAGAGAGTGTGCGTTGTGGAATPAATCCTGTGAC	142
QY	1263	TTTCTTAAAGAGAGATGTTGGTTCCTCCAGCTTGTTGGTGTGTGCAAAACAAAGGATG	1322
Db	141	TTTCTGAAAGAGGAATATGGCGTCCAGAGGTCGTGTGGGTGAGAAATPAAGGGGATG	82
QY	1323	GTTTGAATTAAGATGCTGAGTGGGTTTGGCTCCTCTGAGGAAGATCCTACTCCTGAA	1382
Db	81	GTGAAGAGGAGATGGGAGTGGGTGTGTGATCGCCAGATGAGAGAGATGTGCTGTG	22
QY	1383	TTTGA 1387	
Db	21	CTCGA 17	

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RESULT 5
BG321342
LOCUS BG321342 898 bp mRNA linear EST 27-FEB-2001
DEFINITION D801_07e07_A D801_AAFc_ECCRC_cold stressed Flxweed seedlings
ACCESSION BG321342
VERSION BG321342
KEYWORDS D801_07e07, mRNA sequence.
SOURCE
ORGANISM Descurainia sophia
Eukaryota|Viridiplantae|Streptophyta|Embryophyta|Tracheophyta|
Spermatophytes|Magnoliophyta|eudicotyledons|core eudicotyledons|
rosoids|eurosids II|Brassicales|Brassicaceae|Descurainia.
REFERENCE 1 (bases 1 to 898)
AUTHORS Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J.,
Hattori,J.I., Ouellet,T., Robert,L.S., Sprödt,D. and Tinker,N.A.
TITLE Expressed Sequence Tags from Cold-Stressed Descurainia sophia
Seedlings
JOURNAL Unpublished (2001)
COMMENT Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-Food Canada
KW Nearby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@agr.gc.ca.
FEATURES
source
location/Qualifiers
1..898
/organism="Descurainia sophia"
/mol_type="mRNA"
/db_xref="taxon:89411"
/clone="D801_07e07"
/tissue_type="leaf, stem"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"

```


QY 936 ACCGCCGTGCTCTCGGGTCCCAAAAGTAGCAACAAAATTCCAACACTCTTCGAC 995
 Db 414 ACCGCCATCGTGTTCGGGTCCCGCCAGGTCCGAAACAAAGCCTTCAACGAGGTTCAAC 355
 QY 996 TCGTACCCAACTTAAATGTCCTCCATGTAAAGATGTCATGACCTGATCCTCTGAT 1055
 Db 354 ATGTTTCCGAACCTTAAAGTTTTCACGTGAACACGTGATGATTTGATCCACACTAC 295
 QY 1056 CCGCGTAAACCTCATGGGTGATAGTAACATAGAAATCCAGCTGAGATGATCTCAGAGAG 1155
 Db 294 CCGGGGAAGTGTAGAGGTATGATGATCAATGGACACGAGCTGTGTATGACACGAGAG 235
 QY 1116 TCGACCTTTCTTAAAGCATCCGAAAACCCGAGTATGGCATTAATTTGCAACATATTG 1175
 Db 234 TCGCCGACCTTGAAGAGATCGAAGAACCCGGGTATTTGGCATTACTTGCAAGCGATGTG 175
 QY 1176 CATGTTGTAGTGTGGCATGGGGTTAAGGGGAGTTTAAGTTTGAATTAAGAGAGT 1235
 Db 174 CATGTGTGCGGGGTGGAATGGGAAGAGAGAGGTTTGAATGAGAGGTGAAGAGAGT 115
 QY 1236 GTTTCATTTGTTAATTAATCATGATTTCTTAAAGAAAGATGTTTGTCTCCAGCT 1295
 Db 114 GTGCGTTGTGAATTAATCTTGTGATTTCTGAAGAGAGATATGGCTGCCAGGCTCG 55
 QY 1296 TGTGTGTTGTGCAACAAAGAGATGTTTGAATTAAGATGTTGATGAGT 1348
 Db 54 TGTGTGTTGTGCAAGAAATTAAGGGATGTTGAAAGAGAGATGGGAGATGGGT 2

RESULT 7
 CA839368 684 bp mRNA linear EST 12-DEC-2002
 LOCUS MCT026G05.171831 Ice plant Lambda Uni-Zap XR expression library, 5
 DEFINITION (5:30 PM). Mesembryanthemum crystallinum cDNA clone MCT026G05.5,
 mRNA sequence.

ACCESSION CA839368 GI:26567133
 VERSION CA839368
 KEYWORDS EST.
 SOURCE Mesembryanthemum crystallinum (common iceplant)
 ORGANISM Mesembryanthemum crystallinum (common iceplant)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 Caryophyllales; Aizoaceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 684)
 Cushman, J.C.

AUHTORS An expressed sequence tag database for the common ice plant,
 TITLE Mesembryanthemum crystallinum
 JOURNAL Unpublished (1997)
 COMMENT Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu

PCR PRIMERs
 FORWARD: T3 20mer
 BACKWARD: T7 21mer
 Plate: 026 row: G column: 05
 Seq primer: T3 20mer
 High quality sequence stop: 684.
 Location/Qualifiers
 1..684
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 /db_xref="taxon:3544"
 /clone="MCT026G05"
 /cissue_type="leaf"
 /dev_stage="five-week-old"
 /clone_lib="Ice plant Lambda Uni-Zap XR expression
 library, 5 days 0.5 M NaCl treatment, Crassulacean acid
 metabolism, phase IV (5:30 PM)."

ORIGIN
 /note="Vector: Lambda Uni-Zap XR. Bluescript SK-; Site 1:
 EcoRI; Site 2: XhoI; Library construction was performed
 according to Stratagene's recommended protocol for the
 Lambda UnizapXR vector and cDNA synthesis kit."

Query Match 17.7%; Score 272.4; DB 6; Length 684;
 Best Local Similarity 67.8%; Pred. No. 1,4e-54;
 Matches 381; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 28 CCACCTCAAACTATTTCGAATGCGCTCAGAACCCCAACCTTAAAGCCTTCAAAGCCG 87
 Db 16 CAACCAACACACCTTCTTACATGAACATGCCCCGACACCTTCGCGAAGAGAGCCG 75
 QY 88 GCCCAATGAGCCCAACCTCTCGGCTCAATGTTGGGCGGCTACTAAACCCGCTCA 147
 Db 76 GCCCAATGAGCCCAACCTCTCTAGGAAACATCATGGATGGTCTATTGAACCCACTTA 135
 QY 148 ACGTAGCTCCGCTGAGCTCTCTTACAGCTGCGGGGACTTGTCCAGAGTACATACACA 207
 Db 136 ACTATGATCTCCGTCGCTGATCTCTCGTTGTGTGACTATGCAAGTCACTACAGACA 195
 QY 208 CCTTCATTAACGACCAACACCTCTCTTACCTGCGGCAAGCGGCTACGGAAGCGGAGC 267
 Db 196 GTTTCATCAACGACCCCAACCTCGAGTACTGCGGCTCAGCGCTTACGCAAGCCGAC 255
 QY 268 TACTTCAATTAAGACCCCTTCCCGGGGGCGCAGACCCGTTTGAACGTGTGGCTACTTGT 327
 Db 256 TCTTCGACAAACCGCTTCCCTGATGTGGCGGGCGGCTACGAGCTGTGGATTCCTAT 315
 QY 328 ACGGCATGCGAAGCTCAGCGCTCCAGAGGCGTTTCTGTAAGTCAAGTCCAGGAGAGA 387
 Db 316 ACGTCAACGCGGAGGTAGTACGCGCAAGGCTTTGTTCATTAAGTCAAGCTCGGGGAAA 375
 QY 388 AGTGGATAGGGAATTCGAATTGGAATTGGGTATGTCGTTGTCGAATGACGAGCGATC 447
 Db 376 TGTGGACAAAGAGATCGAATCGAATGGATGTTGTTGTTGACCAATGATGAGCGAGTG 435
 QY 448 GGTGCGCGGACGAAGGAGGTATGTGTGTGAGAGGAGCTTGTAGGGATTATAGT 507
 Db 436 CGAGATATGGAAGAGAGAGATTTATGTGGGTGAGAGGAGACATCCAGAGATTATAGT 495
 QY 508 GGGTTGATGTTCTTGTGCTCAACTTGAATGCTCATCTTGTTCACGACTCAACAA 567
 Db 496 GGGTTGATGCTCTGAGCCTTCGTTGAATCTGCTGAACCTCTCTGTTTGAACCTG 555
 QY 568 CTACTCATGTTGAAGAAGTGA 589
 Db 556 GTTCTGTGTCAGAGAAATGAAGA 577

RESULT 8
 CD397937/c 707 bp mRNA linear EST 07-JUN-2003
 LOCUS Gm_cK18965 Soybean induced by Salicylic Acid Glycine max cDNA 3',
 DEFINITION mRNA sequence.
 ACCESSION CD397937
 VERSION CD397937.1 GI:11455909
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max (soybean)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE 1 (bases 1 to 707)
 Tian,A.G., Wang,J., Cui,P., Han,Y.J., Xu,H., Cong,L.J., Huang,X.G.,
 Wang,X.L., Jiao,Y.Z., Wang,B.J., Wang,Y.J., Zhang,J.S. and
 Chen,S.Y.
 TITLE Characterization of soybean genomic features by analysis of its
 JOURNAL Expressed Sequence tags
 PUBMED Theor. Appl. Genet. 108 (5), 903-913 (2004)
 14624337

COMMENT Contact: Chen S-Y
Plant Biotechnology Laboratory
Institute of Genetics and Developmental Biology, CAS, China
Datun road, Beijing 100101, China
Tel: 86-10-64886859
Fax: 86-10-64873428
Email: sychen@genetics.ac.cn
Email: sychen@genetics.ac.cn
Seq primer: T7 primer.
Location/Qualifiers
1. .707
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/mol_type="mRNA"
/cultivar="Kefeng 1"
/db_xref="taxon:3847"
/r_buase_type="Seedlings"
/dev_stage="two-week seedlings"
/lab_host="X11-Blue MRP strain"
/note="Vector: pBluescript SK+; Site 1: EcoR I; Site 2: Xho I; The cDNA library was constructed by He, C-Y from mRNA isolated from two-week seedlings (cultivar Kefeng 1) treated by spraying 2.0mM salicylic acid for 24, 36, 48 and 72 h. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(AT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into X11-Blue MRP host cells (Stratagene)."

ORIGIN
Query Match 17.6%; Score 271; DB 6; Length 707;
Best Local Similarity 63.7%; Pred. No. 3.1e-54;
Matches 431; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

QY 858 GGTGACAGCCTTGGCGGAGACCTATCATGCTGAGCGGCTTGCACATAGTGAAGATCTC 917
DB 707 GGGGACAGCCTTGGCGGAGACCTTATCATGCTGAGCGGCTTGCACATAGTGAAGATCTC 648
QY 918 ACACAGCAGATCCAGTCAAGCGCGGTCTTCCGGTGCACCAAGTGAAGCAACAAAA 977
DB 647 GTACAGAGGCTCCGCTTACCGCATGCTGTTCGGGTCCCGCAGTGCAGAAACAAGCC 588
QY 978 TTCAACAATCTTTGCACTGTACCCAACTAATGCTCTCCATGTAAAGATGTATC 1037
DB 587 TTCAACAAGAGGTTCGACATGTTCCGAACCTTGAAGTTTGCACGTGAAGACGTATC 528
QY 1038 GACCTGATCCCTCTGATCCCGTGAACCTCATGGGTAACTGAAGTGAAGATGAGCTG 1097
DB 527 GATTGATCCCACTACCTCCGGGAAAGTTGTAAGGTATGATCAATGGGACGAGCTG 468
QY 1098 GAGATCACTGAGGAAGTGCACCTTTCTAAAGACTGCAAAAAACCGAGTGAATGGCAT 1157
DB 467 GTGATACACAGAGAAATGCGCCAGCTTGAAGATCTGAGAAACCGGAGTATGGCAT 408
QY 1158 AATTGCAAGCAATATTCATGTTGTAAGTGTGGCATGGGGTTAAAGGGGAGTTTAA 1217
DB 407 AACTTGCAGGAGTGTGATGTGTGGCGGGGTGAATGGAAGAAAGAGAGATTGGAG 348
QY 1218 GTTCTAAATTAAGAAAGTGTGATGTTTAATAGTCAATGATTTTCTTAAAGAA 1277
DB 347 ATAGAGGTGAAGAGAGTGTGGCTGTGATTAAGTGTGTGAGTTTCTTAAAGAGAA 288
QY 1278 TGTGTGTTCTCCAGCTTGTGGTGTGTGCAAAACAAAGGATGTTTGAATTAAGCAT 1337
DB 287 TATGAGCGTCCAGGAGTGTGGTGTGTGAGAAAGATTAAGGAGTGTGAAGAGGAGAT 228
QY 1338 GGTGAGTGGGTTTGGCTCTCTGAGAGAGATCTTACTCTGAATTTGA-----TTGA 1391
DB 227 GGGGAGTGGGTTGATGCGCCAGATGAGAGATGTGCTGTGCTGGAAGAGATTTGA 168

QY 1392 TAATATTTCATCAGTTTATATTTTAAATTTTACTAATTAATTCATGACATTTATG 1451
DB 167 TTAGCTTAAGCTTGATCTAGAGACTGTAATCTTCATGATGAAACATTTATTC 108
QY 1452 GACATAAGTACTTATTTATATGTTTATTTATTTGAAGTGTTTAAGTTCATATA 1511
DB 107 AATCTTAATCTTCTAATAATGATTTATTTATGTGAGAAATCAAAATTAATAATTTT 48
QY 1512 TTGCAATTAGTTTAA 1528
DB 47 ATATATTTTATGTTTAA 31

RESULT 9
AV784335/c 698 bp mRNA linear EST 28-MAR-2002
LOCUS AV784335 RALV5 Arabidopsis thaliana cDNA clone RALV5-18-J03 3',
DEFINITION mRNA sequence.
ACCESSION AV784335 GI:19803125
VERSION AV784335
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 698)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Aizawa, T., Shibata, K., Shingawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
TITLE Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a Set1/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/planct/index_e.html) for
further details.
JOURNAL COMMENT
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a Set1/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/planct/index_e.html) for
further details.

FEATURES
source
1. .698
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RALV5-18-J03"
/dev_stage="Rosette plants"
/lab_host="SOLR"
/clone_lib="RALV5"
/note="Site 1: Set1; Site 2: XhoI; subjected to
dehydration-created(1,2,5,10,24 hr)"

ORIGIN
Query Match 17.3%; Score 265.4; DB 1; Length 698;
Best Local Similarity 64.7%; Pred. No. 7e-53;
Matches 411; Conservative 0; Mismatches 221; Indels 3; Gaps 1;

QY 753 CCCCAATCACCTTTCACAAAATCTAATGCAAGAACACAACTTCAGACCAACTTAACAA 812
DB 697 CCCCAATCGAATTCATTAAGTGAATGCTACGGTCAAGTTTGAAGCAAGATTAAGAG 638
QY 813 CTAATGACAAATATCAAGAGCAAAACCTTAAGCATTAATTCGCGGTCAAGCTTAGC 872
DB 637 CTTCTGTGAAGTATTAAGAGCAAGAACCGAGCATTTGTGATGACATAGTCTTGGGA 578
QY 873 GCGACACTATCACTGTGAGCGCTTTCAGCATAGTGAAGAA---TTCACAGACCGAGATC 929
DB 577 GCTACAGAGGCTGTTTGGCGCGCTTATGATATAGCTGAGAAACGGTCCAGTGAATGATT 518

Qy	930	CCAGGACAGGGCCGCGGTCTTCGGGGGCCCAAAAGAGGCAACAAAATTCACAACTC	989
Db	517	CCGGTCACTGCTATAGTCTTTGGTGTGTCCACAGTAGAGAAACAGAGCTTCAGAGACGA	458
Qy	990	TTGCACTGTAACCCAAACCTTAATGTCTCCATGTAAAGATGTATCGACTGATCCCT	1043
Db	457	GTAATGAGATCAACAAGAACTTAAGATCTCCATGTAAAGAACACGATTGATCTCTTAATC	398
Qy	1050	CTGATACCGAGAAACCTATGGGTTACGTGAACATAGGAATCGACTGAGATCGACTCG	1109
Db	397	CGATACCAAGGGGACCTTTAGGGTATGTGCACATAGCAATTAACCTTTGTATCATCA	338
Qy	1110	AGGAGTCGACCTTTCTAAAGACATCGAAAAACCCGAGTGTGTCATTAATTTGCAACA	1165
Db	337	AAGAGTCACCGTCTCTAAGCATTCAGAGAAATCAGGGGATGTGCATTAATCTTCAGCG	278
Qy	1170	ATATTGCATGTTGTAAAGTGTGTGTCATGTGGGTTAAGGGGATTTAAAGTTCTAAATAG	1222
Db	277	ATGTTACATGTTGTGCTGGATGTGAATGGGAAGAAAGAACTTTAACTGATGTGAAG	218
Qy	1220	AGAAGTGTGCATTTGATTAAATAGCATGTGATTTTCTTAAGGAAGAAATGTTGGTCTC	1283
Db	217	AGAGATATTGCATTATGTGACAAAGTCATCCAGATCTTGAAGCTGAGTGTTGGTGCA	158
Qy	1290	CCAGCTGTGGGTGTGCAGAACAAAGGATGTTTGAATPAAGATGTGTAGTGCGTT	1345
Db	157	GGATCTTGTGGGTGAGAGAAACAAGACATGATCAAGAACGAAAGATGTGTAAATGGGT	98
Qy	1350	TTAGCTCTCCGAGAGAGATCTCATCTCGTAAT	1384
Db	97	CTTGGCTCCCGTGAAGAAAGAACTGTACTGTAAT	63

JOURNAL
 COMMENT
 Unpublished (2004)
 Contact : Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
 The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castelli
 V., Aury J.M., Jallion O., Wincker P., Penard M., Craud C.,
 Schachter V., Weissenbach J., Salmouat M.
 URGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich Information center for Protein
 Sequences).
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_RF/EST
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.
 Location/Qualifiers
 1. .686

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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotType="Col-0"
/db_xref="taxon:3702"
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/clone_id="Arabidopsis thaliana Adult vegetative tissue
Col-0"

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Query Match	Best Local	Similarity	63.9%;	Score	256.2;	DB	5;	Length	686;		
Matches	420;	Conservative	0;	Mismatches	233;	Indels	4;	Gaps	2;		
QY	732	ACATATATACA	CATCGAGGAT	TCCCAAT	CA	CCCTTCA	CAAAA	CTAAGTGA	GAGAACAA	791	
DB	686	ACATCTATATAGT	AGTATATCA	CCCCCTA	ATCTAAAT	TCTAAT	TCTAAGCTGA	GTCTTCA	CGGTACAG	627	
QY	792	CTTCAGACCAAA	CTCAAA	CACTAAT	ATACAA	AAATATCA	AAAGCGAA	ACCCTTA	AGATACAA	851	
DB	626	TTGTTCACCAAG	ATCAAGAGCTT	CTGTGGA	AGTATAGGA	ACGAAAC	CGAAGAA	TTGTT		567	
QY	852	TTGGCC	-GCTCA	CGACCTTA	GGCGGGA	CACTATCA	GTGTGAG	CGCCCTTCA	CATATAGGA	910	
DB	566	GTTTACCTGGA	CAATGCTTGG	AGCTTA	CAAGAGCTGTT	CTGGCCG	CCCTATATATAG	CTGA		507	
QY	911	GAA---	-TCTCA	CGACCGAGAT	CCCA	GTCA	CGGCGCTT	TCGGG	TGCCCAAA	AGTAG	967
DB	506	GAA	GGTTCCAGTATATAT	GTGTTCCG	GTCACTGTATAT	GTCTTGGTTG	TCCACAG	GTAG		447	
QY	968	CAACAAAAAT	TTCCAA	CACTTT	CGA	CTG	GTACCCAA	CCCTAA	ATGTCTC	ATGTAA	1027
DB	446	AAACAAAGAG	TTGAGAG	ACGA	AGTATAG	ATGATCA	CAAGAA	CTTAA	AGATCCCTCA	GTAA	387
QY	1028	GAATGTATCGA	CTGTATCCCT	CTGTAT	CCCGTAA	ACTATGG	GTATAC	GTAA	CATTA	AG	1087
DB	386	GAA	CA	CGATTTGATCTT	TAATCTCAT	ATCCCG	GGGGA	CTCTTA	GGATGTG	GCATTA	327
QY	1088	AATGACCTG	AATCGA	CACTCGA	GAAGTGA	CACTTCTTA	AAAGCA	CTCGAAAA	CCGAG		1147
DB	326	AAT	AAACTTGTGTAT	CGATACAA	AGAA	GTCA	CCGTTCC	TAA	GCATTC	AAAGAA	267
QY	1148	TGATTTGCAT	TAATTTGCA	AGCAATTTG	CAATGTTG	TAAAGTGTG	GGATG	GGCATG	GGGTTAA	GGG	1207
DB	266	GGATTTGC	ATATCTTCA	GGGAGAT	GTTA	CAATGTTG	TAGCTGA	AGATGGAA	GGAA	GG	207
QY	1208	GGAGTTTA	AGGTTTAATA	TAAAGAG	AGTGTG	CACTTGGTTA	TAAATG	CTATGATTT	CT		1267
DB	206	AGAGCTTA	AACTGATG	TTAAGAA	AGATTTG	CACTTGTGA	CAAGCTAT	CGAGTT	CTT		147
QY	1268	TAA	GGAATAG	AGATTTG	GTCTCTCA	AGCTTGGTGTG	TGAGAA	CAAA	GGAGATG	TTT	1327
DB	146	GAA	AGCTGA	AGTTTGTG	GCAGAG	CTTGTGTGGT	TAGAA	GAACAA	GGAGACTG	ATCA	87
QY	1328	GAA	TAAAGATG	TGTAGTGG	TTTGGCTCC	CTCGA	GAAGATCT	CTA	CCTGA	TT	1384
DB	86	GAA	CGA	ATGATGTGA	TGGTTCTCG	CTCCGCTTGA	AGAA	CACTGA	CTGA	TT	30

RESULT 11					
AM774539/c					
LOCUS	AM774539	648 bp	mRNA	linear	EST 07-SEP-2000
DEFINITION	EST333690 KV3 Medicago truncatula cDNA clone pKV3-22L18, mRNA sequence.				
ACCESSION	AM774539				
VERSION	AM774539.1	GI:7718456			
KEYWORDS	EST.				
SOURCE	Medicago truncatula (barrel medic)				
ORGANISM	Medicago truncatula				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.				

fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

ORIGIN

Query Match 16.1%; Score 248.4; DB 2; Length 623;
Best Local Similarity 66.0%; Pred. No. 8.8e-49;
Matches 406; Conservative 0; Mismatches 202; Indels 7; Gaps 3;

Qy 749 GATATCCCAATACACCTTTCACAAATTAAGTGAAGAACACAACTTCAGACCAACTCA 808
Db 612 GACACCAAAATCCCTCTTTCCCATCCAGGAGAAAGAGAGCTTCAGGCCCACTCAAA 553
Qy 809 ACAACTAATGACAAATTCAGAAAGCAAACTTAAGCTTAACATTCGCCGGTCAAGCCT 868
Db 552 TCCCTTA---CAACATTAACAGCTCTGAGAACCCAGCTTGTTCAATCGTGGGCAAGCAT 496
Qy 869 AGGGGCGACATATCAGTCGTGAGAGGCGCTTGAACATAGTGAGAAATCTACAGCCAGAT 928
Db 495 CGGGGCAACCTATTCATCTGAGAGCGCTTGAACCTGATCGAAACGGGGTAAAGAGAT 436
Qy 929 CCCAGTCAGGCGCGTGTCTTCGGGTGCCCAAAAGTAAAGCAAAATTCACAACT 988
Db 435 CCGGTCACCGCCATCGTGTTCGGGTCCCGCAGGTGAAACAGAGCTCAAGAGAG 376
Qy 989 CTTCGACTCGTACCAAACTTAATGCTCTTCATGTAAGAAATGTCATGACTGATCCC 1048
Db 375 GTTCAACATGTTTCCGAACCTGAAGATTTCACGTGAAGAACGTATCGATTGATCCC 316
Qy 1049 TCTGTATCCCGTGAACATCAGGTGATGTAAGTAAATGAGTGAAGTGAAGTGAATC 1108
Db 315 ACACCTACCCGGGAAAGTTTGAAGGTATGATGACGCGACCGAGCTGTGATAGACAC 256
Qy 1109 GAGGAAGTCGACCTTCTTAAGAGACTCGAAACCCAGTATGTCATTAATTTGCAAGC 1168
Db 255 GAGGAAGTCGCGGAGCTTGAAGAGACTCGAGAACCCGGGTATTTGGCATTACTTGCAAGC 196
Qy 1169 -AATATTGATGTTG---TAAGTGTGGCATGGGGTTAAGGGGAGTTTAAGTTGTA 1224
Db 195 GNATGTTGATGTTGGGTGGCGGGGTGGAATGGAGAAAGAGAGATTTAAGATGAGGG 136
Qy 1225 ATAAGAGAGTGTGATGTTTAATAGTCATGATGATTTCTTAAGGAAGAAGTTTG 1284
Db 135 TGAAGAGAGTGTGCGGTGTAATTAAGTCTTGATGATTTCTGAAGAGAGAAATGAGCG 76
Qy 1285 TTCCCTCAGCTTGTGGGTGTGTCAGAAACAAAGGATGTTTGAATTAAGATGATGAGT 1344
Db 75 TGCCAGGGTCTGTGGGTGAGAAAGATTAAGGGATCTGAAGAGGAGATGGGAGT 16
Qy 1345 GGGTTTGGCTCTC 1359
Db 15 GGGTGTGATGATGCGC 1

RESULT 13
CV708865/c 744 bp mRNA linear EST 03-NOV-2004
LOCUS UCRPT01.0011p17.f Poncirus trifoliata CTV-challenged cDNA library -
DEFINITION AG12 Poncirus trifoliata cDNA clone PT_65a0011p17, mRNA sequence.
ACCESSION CV708865
VERSION CV708865.1 GI:55291233
KEYWORDS EST.
SOURCE Poncirus trifoliata
ORGANISM Poncirus trifoliata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Sapindales; Rutaceae; Poncirus.

REFERENCE 1 (bases 1 to 744)
Roose, M.L., Ye, X., Federici, C.F., Close, T.J., Fenton, R.D.,
AUTHORS Mamamaker, S., Kilm, H.R., Kudrna, D. and Stum, D., Wiscofski, M.,

TITLE
JOURNAL
COMMENT
Wing, R.
Development of EST Resources and New Genetic Markers for California
Citrus - Poncirus trifoliata CTV-challenged phloem - AG12
Unpublished (2004)
Contact: Mikeal Roose
Department of Botany & Plant Sciences, University of California
Riverside, CA, 92521-0124, USA
Tel: 9097874137
Fax: 9097874437
Email: mikeal.roose@ucr.edu
Seq primer: T7

FEATURES

source

1..744
/organism="Poncirus trifoliata"
/mol_type="mRNA"
/cultiivar="Pomeroy OP"
/db_xref="taxon:37690"
/clone="PT_65a0011p17"
/tissue_type="Phloem"
/dev_stage="10 - 30 cm shoots"
/lab_host="E. coli TUC121"
/clone_1lb="Poncirus trifoliata CTV-challenged cDNA
library - AG12"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the
greenhouse at University of California, Riverside. The
action was an open-pollinated (very probably selfed)
seedling of Poncirus trifoliata cv Pomeroy that was
selected as homozygous for the CTV resistance gene. The
rootstock was sweet orange infected with citrus tristeza
virus (CTV) isolate T514 over 1 year before sampling (CTV
infected sweet orange, but not genotypes carrying the CTV
resistance gene). Shoots 10-30 cm long were harvested in
October 2000, and the green phloem (bark) was removed and
frozen quickly in dry ice. Total RNA was extracted using
TRIzol reagent (Gibco). Poly(A) RNA was purified, a cDNA
library was made, and 0.5 million primary lambda cDNA
clones were in vivo excised to give a population of
phagescript SK(-) phagemids. All steps to this point were
performed in the ML Roose lab at the University of
California, Riverside by X. Ye. Phagemids were plated,
plasmid DNA purified, cDNA clones archived, and DNA
sequences determined bi-directionally using an ABI3730 at
the Arizona Genomics Institute, University of Arizona
(Kilm, Kudrna, Stum, Wiscofski, Wing). Chromatogram files
were downloaded to UC Riverside (Close), then processed at
UC Riverside (Mamamaker) using the HarvEST pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to a
high quality region. Sequences that retained a phred 17
region of at least 100 bases were deposited to GenBank."

ORIGIN

Query Match 16.1%; Score 247.8; DB 7; Length 744;
Best Local Similarity 65.8%; Pred. No. 1.3e-48;
Matches 360; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

Qy 852 TTGCGGTCACAGCCTTAGGCGGACACTATCAGTCGTGAGCGGCTTCGACATAGTGAG 911
Db 742 TTCAAGGAGCATATTTGGGTGCGAGCTGTCAATTTTAAGCGCTTTGATTTGGCTGA 683
Qy 912 AATCTCAGACCGAGATCCGAGTCACGCGCGTGTCTTTCGGGTGCCCAAAAGTGAAGC 971
Db 682 AATGGGTGACTGACATCCCTGTGGCGGCGTGTGTTCGGTTCACCAAGTTGGGAGC 623
Qy 972 AAAAATTCACCAACTCTTGACTCGTACCCAAACCTAAATGCTCTCATGTAAGAAAT 1031
Db 622 AAAGCATTTAAAGAAAGTGAAGAGTACACGAACGTGAAGATTGACAGTGAAGAAC 563
Qy 1032 CTCATCAGCAGATCCCTGTATCCGCTGAACCTCAAGGTTTACGTGAACATAGGATC 1091
Db 562 ACATTATTCATACGACCTACCCGGGAGGTTGCTGGGTACGTTAAACGGGAGCT 503

	RESULT 14
LOCUS	BQ989600
DEFINITION	BQ989600 BQ989600 .yg.abl.QG_EFGHU lettuce serricola Lactuca sativa cDNA clone
ACCESSION	OGC18822.yg.abl.QG_EFGHU lettuce serricola Lactuca sativa cDNA clone
VERSION	BQ989600.1 GI:22409135
KEYWORDS	EST.
SOURCE	Lactuca sativa
ORGANISM	Lactuca sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichoriaceae; Lactuca. 1 (bases 1 to 696) Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesberg,L., Lai,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K. lettuce and Sunflower ESTs from the Compositae Genome Project http://compenomics.ucdavis.edu/ Unpublished (2002) Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Ammundson Hall, UCD, Davis, CA 95616, USA Tel.: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@erc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_Ca_contig3754, see http://cgdb.ucdavis.edu/ for details.
JOURNAL COMMENT	Plate: QGF18 row: B column: 22.

size bias. Details of each source of RNA and library construction can be obtained at http://cgpd.ucdavis.edu/TAG_TISSUE-leaves_dark_grow
TAG_L1B=QG_EFGHJ lettuce *serriola*
TAG_SEQ=GCTAGTCGGG"

Query Match	14.9%	Score 228.6	DB 5	Length 696
Best Local Similarity	61.2%	Pred. No. 5.4e-44	Mismatches 234	Indels 0
Matches 369	Conservative 0	Gaps 0		
Qy 653	AGGTTCCGGCGTCCCAAGACAAAGGAAAGGAGGACGAGACGATGATGACGACCCCA	712		
Db 92	AGATTCAAGGCGAGCTTGACGACACGACGAGGATGATGACACAGATGAAATTCGAG	151		
Qy 713	AGTGATCAAGGTTGATGACAAATATACATCCGAGGATCCCAATCACCCTTACAAA	772		
Db 152	GGTATATCAGGGTTGGCTTAACGATTTACCTCGAGATGATCGAATTCGCTTTCACAAA	211		
Qy 773	ACTAAGTCAAGAACCAACTTCAAGCCAACTCAAACTAATGACAAATATCAAAA	832		
Db 212	ACAAAGGTAAAGAACAAAGTGTGACAACTATCAAACTTGGTGGGCACTTCAAAA	271		
Qy 833	CGAACCCTAAGCATATTCGGCGGTCAAGCTTGGCGCGACATATAGTCGTAG	892		
Db 272	CGAAGAACTAAGCATATTCGACCGGACATCTCCCTGGGTGCAAGTTATGATCTTATC	331		
Qy 893	CGCCTTCGACATAGTGAGAAATCTCAGACCGAGATCCCACTACGCGCGTCTTCGG	952		
Db 332	CGCCTTCGATCTAGCAAAAACGAAATCAAGAGATGCCAATTCGCGCTTCGCTTCGG	391		
Qy 953	GTECCCAAAAGTAGGCAACAAAATTCACAACAATCTTCGATCGTACCCAACTTAA	1012		
Db 392	TTCTCTCAAGTGGCAACCAAGCATTCACAGATCGTCTTAAACAATTCCTCAATGTCAA	451		
Qy 1013	TGTCTTCGATGTAAGAAATGTCATCGACCTGATCCCTCTGTATCCCGTAAATCATGGG	1072		
Db 452	AATCTTTCACATTTAAACCAAGATCGATCTTATTCGCTATACCAAGTGGGTTACTCGG	511		
Qy 1073	TTACGTGAACATAGGAATCGAGCTGGAGATCGACTCGAGGAAGTCGACCTTTCAAAAGA	1132		
Db 512	GTAAGTGAACACCGGTGTAGTTTCGTGATCGATCAACAGAAAGCTTCGAGCTTGAAGA	571		
Qy 1133	CTCGAAAAACCCGAGTATTTGCAATATTTTGCAGACAAATATTCGATTTGTAAGTGGTGG	1192		
Db 572	GTCGACGAACATCTGGAAGATCGGCACTAATTTTGCAGGGGATGTGACGTTGAGCTGGGTTG	631		
Qy 1193	GCATGGGGTTAAGGGGAGTTTAAGGTTGTAATTAAGAAAGTGTGATGGTTAATTA	1252		
Db 632	GAATGGGAGGATGTGATTTGAATTAAGAGTGAATCGGAGCTTGTCTTGTGATGAATAA	691		
Qy 1253	GTC 1255			
Db 692	ATC 694			

RESULT 15
BO989130
LOCUS BO989130 697 bp mRNA linear EST 21-AUG-2002
DEFINITION OGF16M11.yg.ab1 QG_EFGHJ lettuce *serriola* Lactuca sativa cDNA clone
ACCESSION BO989130
VERSION BO989130.1 GI:22408665
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Lactuca sativa
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 697)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,

Result No.	Score	Query Match	Length	DB	ID	Description
1	1311.5	55.0	412	2	A84857	probable lipase [
2	789.5	33.1	419	2	T04551	hypothetical prot
3	770.5	32.3	423	2	C86198	hypothetical prot
4	703.5	29.5	527	2	F96552	hypothetical prot
5	686.5	28.8	447	2	G84789	probable lipase [
6	670	28.1	515	2	H86202	hypothetical prot
7	616	25.8	355	2	E84716	probable lipase [
8	606.5	25.4	529	2	A86428	probable lipase [
9	442.5	18.6	601	2	E71435	probable triacylg
10	435	18.2	484	2	H84723	probable triacylg
11	412.5	17.3	471	2	E86132	hypothetical prot
12	404	16.9	357	2	T01607	probable triacylg
13	162.5	6.8	407	2	S76637	hypothetical prot
14	131.5	5.5	805	2	T06657	hypothetical prot
15	121	5.1	1264	2	S64146	probable membrane
16	114	4.8	320	2	T30894	lipase homolog T
17	110.5	4.6	421	2	T33811	hypothetical prot
18	106	4.4	1187	2	F86422	carbamoyl-phosphat
19	105	4.4	300	2	T33232	hypothetical prot
20	105	4.4	353	2	T27800	hypothetical prot
21	104.5	4.4	737	2	H95882	probable aldehyde
22	104.5	4.4	1434	2	C82933	DNA-directed RNA
23	103.5	4.3	353	2	T27759	hypothetical prot
24	102	4.3	392	2	UQ1350	triacylglycerol 1
25	101	4.2	900	2	T50773	translation initiat
26	101	4.2	1279	2	A47363	RNA helicase A -
27	99.5	4.2	614	2	T06741	hypothetical prot
28	99.5	4.2	900	2	T47732	probable translat
29	99.5	4.2	4589	2	T14914	dynamin beta heavy

30	99	4.2	297	2	JT0604	heat shock protein
31	99	4.2	869	2	S3533	hypothetical prote
32	98.5	4.1	336	2	T23222	hypothetical prote
33	98.5	4.1	1240	2	B75053	DNA polymerase II
34	98.5	4.1	1240	2	B742050	DNA polymerase II
35	98	4.1	371	2	H70326	hypothetical prote
36	97.5	4.1	802	2	B84560	hypothetical prote
37	97	4.1	865	2	A83946	DNA mismatch repa
38	97	4.1	1912	2	S68176	TGG protein - hum
39	97	4.1	2331	2	S44054	genome polyprotein
40	94.5	4.0	374	2	D24827	heat shock 82k pr
41	94	3.9	307	2	T27061	hypothetical prote
42	94	3.9	737	2	AH1958	hypothetical prote
43	94	3.9	1099	2	C72363	carbamoyl-phosphat
44	94	3.9	4096	2	A57099	DNA-methylated pro
45	93.5	3.9	238	2	T27044	hypothetical prote

ALIGNMENTS

RESULT 1

Probable lipase[imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: A84987
 R:Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moflett, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Talion, L.;
 Euseb, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84857
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-412 <STO>
 A:Cross-references: UNIPROT:Q9SUJ7; UNIPARC:UPI000004664; GB:AE02093; NTD:g4512683; PI
 CGenetics:
 A:Gene: At2g42690
 A:Map position: 2

[illegible]

Oy 435 LAPPEEDPTPEF 446
 Db 401 LAPVEEPEVPEF 412

RESULT 2

T04551
 hypochemical protein F28J12.210 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T04551
 R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, February 1998
 A:Reference number: 215377
 A:Accession: T04551
 A:Molecule type: DNA
 A:Residues: 1-419 <BEV>
 A:Cross-references: UNIPROT:O49523; UNIPARC:UPI000004897F; EMBL:AL021710
 C:Genetics:
 A:Map position: 4
 A:Introns: 83/3; 211/3; 288/2
 A:Note: F28J12.210

Query Match 33.1% Score 789.5; DB 2; Length 419;

Best Local Similarity 37.8%; Pred. No. 2.8e-557; Indels 63; Gaps 8;
 Matches 168; Conservative 77; Mismatches 137;

Oy 17 WPELLGSNAGALNPLNDELRELLRCGDFCQVYDTFTINDONSSYCGSSRYGKADLLH 76
 Db 23 WRDLSGQNMKGMQLPDLQDLREYIHYGEMAGQYDTFTINTESQFAGASISKDPFA 82
 Oy 77 KT---APFGADRFDVAVLYATKAVVPEAFLLKSREKMDRESNIGYVVSNDERS 132
 Db 83 KVGLEIAPH--YTKKVKTFIYATSDIHVPSFLLPFISSRGWSKESNMGVAVTDDQG 140
 Oy 133 SRVAGREVVVVRGTCRDYEWDVYGAQLESAPHLRTQTTHVEKVENEEKSIHSS 192
 Db 141 TALGRKRIVVSKRSQVPLEWEDFEGLVNA----- 173
 Oy 193 WYDFENILGASAKDKGSGDDDDPKVMQGMNTIYTSBDPKSPFTKLARSQTOLTK 252
 Db 174 -----IKIFG-----ERNDOVQIHQGVSYLSGQDBRSPTTKTNARDQVARE 215
 Oy 253 LKQMTKTKKDELTSTFGHSLGATLSVSAFDIYEN-----LTTEIPTAVVPECP 304
 Db 216 VGRLEKTKXDEBSITICGHSIGALATLSATDIVANGVNRKSRPDKSCPVTAFVFSAP 275
 Oy 305 KVGKKFQOLFDSYVNLVLRNVYIDLPLYPVLMGVNIGILEIDSRKSTFLKDSK 364
 Db 276 RVGDSDFPKLPSGLEDIRLRLNLPDIPIYPP--IGSEVGDFPDIIDTKSPYMKSPG 333
 Oy 365 NPSDMNLQALILHVVGSMHGV-KGE-FKVNKRKSVVALVNSCDFLKEBCLVPPAMVVQN 422
 Db 334 NLATHTCLEGLYHGAAGTGNKADLPRLDVERAIGLVNKSVDGLKDCMVPGKKRVLKN 393
 Oy 423 KGMVLNKDGEVNLAPPEEDPTPEF 447
 Db 394 KGMVQDDGSGWELVHEIDNEDLD 418

RESULT 3

C86198
 hypochemical protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: C86198
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huitzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maitl, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-423 <STO>
 A:Cross-references: UNIPROT:Q9LNC2; UNIPARC:UPI00000481DD; GB:AE005172; NID:g8844130; PII C:Genetics:
 A:Map position: 1

Query Match 32.3% Score 770.5; DB 2; Length 423;

Best Local Similarity 37.0%; Pred. No. 9.2e-54; Indels 55; Gaps 6;
 Matches 163; Conservative 73; Mismatches 150;

Oy 17 WPELLGSNAGALNPLNDELRELLRCGDFCQVYDTFTINDONSSYCGSSRYGKADLLH 76
 Db 9 WKVLSGQNMKGMQLPDLQDLREYIHYGEMAGQYDTFTINTESQFAGASISKDPFA 68
 Oy 77 KTAPE-PEGADRFDVAVLYATKAVVPEAFLLKSREKMDRESNIGYVVSNDERSRV 135
 Db 69 RTGFLKANPFRYKTKYIYATASIKLPISEIVKSLSDASRVQTNMGYIAVATDQKAM 128
 Oy 136 AGREVVVVRGTCRDYEWDVYGAQLESAPHLRTQTTHVEKVENEEKSIHSSMYD 195
 Db 129 LGRDVIYVNRGTLQPYEMANDPFLPEPA-----IS 160
 Oy 196 CFNINILGASAKDKGSGDDDDPKVMQGMNTIYTSBDPKSPFTKLARSQTOLTKQ 255
 Db 161 VFPT-----DPKONPRIISGQWLDIYASDSRSPYDTTSAQEQVGEIKR 205
 Oy 256 LMTKYKQETLSITFGHSLGATLSVSAFDIY-----ENLT-----TTEIPTAVVPECP 306
 Db 206 LLELYKDEBSITFTGHSIGAVMSVLSADLVGKKNNININLQKQVPIVFAFGSPRI 265
 Oy 307 GNKKFQOLFDSYVNLVLRNVYIDLPLYPVLMGVNIGILEIDSRKSTFLKDSKNP 366
 Db 266 GDNHFNKNVDSLOPRLNLRNVYDVAHPYLLI--YSEIGVEILEITLNTSTYKRLNF 323
 Oy 367 SDMNILQALILHVVGSMHGVKEPKVNVKRKSVVALVNSCDFLKEBCLVPPAMVVQN 426
 Db 324 RNYTNLLEIYHGMAGMDDTGQVFLKEIGRDISLVNKGDLAKDEYLPSTRCIANGM 383
 Oy 427 LNKDGEVNLAPPEEDPTPEF 447
 Db 384 QMDGTWKLTVNRDHDVD 404

RESULT 4

F96552
 hypochemical protein F5D21.19 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: F96552
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huitzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maitl, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F96552
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-527 <STO>
 A:Cross-references: UNIPROT:Q9CBJ6; UNIPARC:UPI000009D534; GB:AE005173; NID:g10092365; P

C:Genetics:
A:Gene: F5D21.19
A:Map position: 1

Query Match 29.5%; Score 703.5; DB 2; Length 527;
Best Local Similarity 35.5%; Pred. No. 2.9e-48;
Matches 168; Conservative 69; Mismatches 133; Indels 103; Gaps 14;

QY 17 WPELGSNMAAGLNLDELRELLRCGDFCQVYDTFTINDONSVCSSRGKADL 74
DB 91 WREVGCGNMEGQDDPNNHLRREIRYGEPAQCYSPDFDPSPKTCGSCKHPDSFPL 150
QY 75 ----LHKTAFPGGADRFVVAALYATAKVSVPFAFLKSRREKMRRESNMIGYVVS 129
DB 151 NLDLHLK-----GTTIRYKATSNINLPN-FFQKSLSSINQHANNMGFAVAT 201
QY 130 D--ETSRVAGREYVYVWRCGRDYEWVDVLAQLESANPLLTQOTTHEKVENEEKS 187
DB 202 DEEVSRL-GRDIVAMRGVTYLEWV----- 228
QY 188 IHKSMWDCRNILSGASKDGKSGDDDDDDPKVMQGMWTTITSEDPKSPFTKLSART 247
DB 229 ----YDL-----KDIICSANFGDDPSIKIEGFHDLTYTKEDSCKFSFARB 272
QY 248 QLOTKLKQMTKXKYD-----TLSTTFAGHSLGATLSVSAFDIYE--NL-----TTELPV 296
DB 273 QVLAELVKRLIRYGTETEEGKHTSITVTGHSLSGSLAVSAVDLDELNLNHNVPENNYKIP 332
QY 297 TAVVFGCPKVGKPKFQQLFDSYPMNLVYHVNVDLPLYPVKL----- 340
DB 333 TVFSFGSPRVGNLAFKRCDEL-GVKVLRYVNVHDKVPVGVGIPTEKQFOKVEEKTS 391
QY 341 --MGVYVIGIELEIDSKSTFLKDSKPSDMHNLQALIHVSGMVGKGE---FKVYVK 394
DB 392 FPMYSAAHVGVELADHKKSPEFLKPTKDCGCHNLEALHLVDGNGHDEBEAKRFLCVTK 451
QY 395 RSVALVKSQDFLKEECGLVPPAMVYVONKGVNLKDGEMV--APPEEDPTPE 445
DB 452 RDLALVKSQDFLKEGTHVPPCMKDEKGMVKNKGDDGMVLPDRPLEPHGPE 504

RESULT 5
G84709
probable 11page (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: G84709
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Unayam, L.; Tallon, L.; eues, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84709
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-447 <STO>
A:Cross-references: UNIPROT:O04340; UNIPARC:UPI00000485C5; GB:AE002093; NID:g1946364; PIR C:Genetics:
A:Gene: At2G30550
A:Map position: 2

Query Match 28.8%; Score 686.5; DB 2; Length 447;
Best Local Similarity 35.6%; Pred. No. 5.2e-47;
Matches 160; Conservative 78; Mismatches 133; Indels 79; Gaps 14;

QY 16 TWPELGSNMAAGLNLDELRELLRCGDFCQVYDTFTINDONSVCSSRGKADL 75
DB 22 TWRIQGEQDDWAGLMDMDPLRSELIRYGEWAQCYDAFDPSPKTCGSTRRLHFF 81
QY 76 HKTAFPGGADR-PPVVAALYATAKVSVEAFLKSRREKMRRESNMIGYVVSNDTSR 134
DB 82 DSL---GMIDSGEVARLYATSNINLPN-FFSKSRMSKVMKANNMGYAAVDDTSR 137

QY 135 -VAGREYVYVWRCGRDYEWVDVLAQLESANPLLTQOTTHEKVENEEKSIHKS 193
DB 138 NLRGRDIALAMGTATYKLEMIADLKDYKPV-----TENKIR----- 175
QY 194 YDCFNINLGSASKDKGSGDDDDDDPKVMQGMWTTITSEDPKSPFTKLSARTQTKL 253
DB 176 --C-----PDPVAVKESGFLDLYTDKDTCKPARFSAREQILTEV 213
QY 254 KQMTKXKYD-----TLSTTFAGHSLGATLSVSAFDIYE--NLTE---IPVAVVGCP 304
DB 214 KRLVEHGGDDDDSLITVTGHSLSGALATLSAYDLAEMRLNKSCKGVLPVTLTYGCP 273
QY 305 KVGKPKFQQLFDSYPMNLVYHVNVDLPLYPVKLWG-----YVNI 347
DB 274 RVGNVRRREMSEL-GVKVRVNVNVHDVPSKQLFLNESRPHAMKLAGLPMCYSHVG 332
QY 348 IELEIDSKSTFLKDSKNPSDMHNLQALIHVSGMVGKGE-FKVNKRSVALVKSQDF 406
DB 333 EELALDHQNSPFLKPSVDVSTAHNLBAMHLHDGHHG-KGERFVLSGRDHALVKNKASDF 391
QY 407 LKSECLVPPAMVYVONKGVNLKDGEMVLA 436
DB 392 LKSEHLQIPFPWRDANKGMVNRNSEGRWIOA 421

RESULT 6
H86202
hypothetical protein (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86202
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Greasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hutzar, L.
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.-C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Malt, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, L.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86202
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-515 <STO>
A:Cross-references: UNIPROT:Q9W9Y7; UNIPARC:UPI00000481E6; GB:AE005172; NID:g7523699; PIR C:Genetics:
A:Map position: 1

Query Match 28.1%; Score 670; DB 2; Length 515;
Best Local Similarity 35.1%; Pred. No. 1.3e-45;
Matches 157; Conservative 73; Mismatches 141; Indels 76; Gaps 12;

QY 16 TWPELGSNMAAGLNLDELRELLRCGDFCQVYDTFTINDONSVCSSRGKADL 75
DB 88 TWRIQGEQDDWAGLMDMDPLRSELIRYGEWAQCYDAFDPSPKTCGSTRRLHFF 147
QY 76 HKTAFPGGADRFPVVAALYATAKVSVEAFLKSRREKMRRESNMIGYVVSND-ETSR 134
DB 148 DSLGIISG--YVARLYATSNINLPN-FFSKSRMSKVMKANNMGYAAVSDNATR 204
QY 135 V-AGREYVYVWRCGRDYEWVDVLAQLESANPLLTQOTTHEKVENEEKSIHKS 193
DB 205 CRLGRDIALAMGTATYKLEMIADLKDFLPV-----SGNG 240
QY 194 YDCFNINLGSASKDKGSGDDDDDDPKVMQGMWTTITSEDPKSPFTKLSARTQTKL 253
DB 241 FRC-----PDPVAVKESGFLDLYTDKDTCKPARFSAREQILTEV 280
QY 254 KQMTKXKYD-----ETLSTTFAGHSLGATLSVSAFDIYE--NLTE---IPVAVVGCP 304

Db 281 KRLVRYGDEBGEELSTVTGSHLSGALAVLSAADVAMGVNRTRKGVIPVTAFTYGGP 340
Qy 305 KVGKKKQQQLFDSYPNLVNLVHVRVVIDLPLYP-----VKLMG-----YVNI 347
Db 341 RVGIRFERERLEKT-GVAVLVVNEHDVAVKSPGLFLNERAPQALMKLAGLPMCTSHVG 399
Qy 348 IELEIDSRKSTPLKDSKRNPSDMNLQALILHAVSGHVGKGFVKVNRKSVLVKSCDFL 407
Db 400 EMLDLDHQKSPFLKPTVDLSTAHNLDELHLLDDGTHGKGFVLSGRDPALVVKASDFL 459
Qy 408 KEBCLVPPAMVNVONKGMVNLKDEGW 434
Db 460 KDHFVVPVYRQDANKGVNRYTDRMI 486

RESULT 7

probable lipase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B44716
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beilto, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umagam, U.; Tallon,
L.; euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
J. Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617157
A:Accession: B84716
A:Status: Preliminary
A:Molecule type: DNA
A:Reads: 1-355 <STO>
A:Cross-references: UNIPROT:O82274; UNIPARC:UP100000485CD; GB:AE002093; NID:g3746065; P1
C:Genetics:
A:Gene: Atg31100
A:Map position: 2

Query Match 25.8%; Score 616; DB 2; Length 355;
Best Local Similarity 32.9%; Pred. No. 1,6e-41;
Matches 146; Conservative 69; Mismatches 111; Indels 118; Gaps 8;

Qy 17 WPELISNAGLNLPLNDELRELLRCGDFCQVYTFINDONSYYGSSRYGADLLH 76
Db 9 WKELSGSKMDLPLDLRLRYILHYGDMAEII-----AATPKKSLLE 54
Qy 77 KTAFFGADRFDVAVYLATAKVSYPEAFILKSRREKMDRESNMIGVAVVNSDTSVA 136
Db 55 P-----VTSKPTL-----SDEGKKLL 70
Qy 137 GRREYVVMRGTCRDYEWVDVLAQLESAPLARTQOTTHVEKVENEEKSIHKSWSYDC 196
Db 71 GRRGVAVMRGTIOLEWANDDPPLPSA----- 99
Qy 197 FNINILGSAKDKGSDDDDDDDPKVMGMMTITSEDPKSPFYKLSARTOLQTKLKOL 256
Db 100 -VWVFPGA-----NPMDPRVANGMVSLTSTDPSPRPKTSAOEVOBELRL 147
Qy 257 MTKYDELSTTFAGSILGATLSVSAFDIYEN-----LTIDIPYAVFEGCPKYN 308
Db 148 LELYNEBVTTTLTHSLGAVMSILSADFLNHEPKTTPSLQSHLCVTPAFSGPQIGD 207
Qy 309 KKFQOLFDSYPNLVNLVHVRVVIDLPLYPVKLMGVNIGIELEIDSRKSTPLKDSKNSPD 368
Db 208 RSFKRLVSLSHLHLRLTNPDLIPRPV--FRFTDIEBELQINTLSEVYKSLNIGH 265
Qy 369 WHNLOALILHAVSGHVGKGFVKVNRKSVLVKSCDFLKEBCLVPPAMVNVONKGMVNL 428
Db 266 FHNLEAVLHGVAGTQHNQGEFLIEINRDIALVNLGLDALEDKYLVPGHMVVLENGVQS 325
Qy 429 KDGKVV-----APREDPTPE 445
Db 326 DDGTWKLNGDRSKKKQEEDEKEE 349

RESULT 8

probable lipase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86428
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzer, L. Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltz, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86428
A:Status: Preliminary
A:Molecule type: DNA
A:Reads: 1-529 <STO>
A:Cross-references: UNIPROT:Q9C8G6; UNIPARC:UP100000482FD; GB:AE005172; NID:g11055819; P1
C:Genetics:
A:Map position: 1

Query Match 25.4%; Score 606.5; DB 2; Length 529;
Best Local Similarity 32.0%; Pred. No. 1,7e-40;
Matches 151; Conservative 79; Mismatches 157; Indels 85; Gaps 15;

Qy 1 MAEAQPLGSKPGPTPELISNAGLNLPLNDELRELLRCGDFCQVYTFINDON 60
Db 104 MTPAAS--REKISKMRRELGSNMNLPLDPLHWRRETKXGEFVESYSLDPL 161
Qy 61 SSYCGSSRYGADLLHKTAPFGADR--FDVAVLVYATKVSYPEAFILKSRSEKMDRE 118
Db 162 SEFCSSRYNKNKLFEEL---GLTRGIVYTKIYMSKVDVDPWF--LSSALGETSKD 216
Qy 119 SNMIGYVNSDSTSVAGRRVYVVRGTCRDYEWVDVLAQLESAPLARTQOTTHVE 178
Db 217 SNMIGFVAVSGDRSLNIGRDIYVAVRGVTPPEWMDLRTSMEP----- 262
Qy 179 KVNEEEKSIHKSWSYCCFNINILGSAKDKGSDDDDDDDPKVMGMMTITSEDPKS 238
Db 263 -----FPC-----EGK-----HGKTVVYQSGFLSYNKSLELT 291
Qy 239 PFTLSARTOLQTKLKMLTKYD--ETLSITFAGSILGATLSVSAFDIYENLTTEIP- 295
Db 292 RYNRESASEQTMDEVKLVNFFKDRGEVSLITGHSLGALALMAHYEAR---DVPA 347
Qy 296 ---VTAVVFGCPKVNKKFQQLFDSYPNLVNLVHVRVVIDLPLYP-----VKLMG----- 342
Db 348 LSGNISVIFGAPRVGNLAFREKLSNL-GVAVLVVVKODIVPFLPGVFNKVLNKLNPI 406
Qy 343 -----YVNI GIELEIDSRKSTPLKDSKRNPSDMNLQALILHAVSGHVGKGFVKVNR 395
Db 407 TSLNMYRVRHVGTQLKDVESSPYKRDSDIGRAHNLEEVYLVHVDGFRKKSGRVAVAR 466
Qy 396 SVLVKNSCDFLKEBCLVPPAMVNVONKGMVNLND-GEWV--LAPREDPTPE 444
Db 467 DVASVNSTDWLIDLHLRIPEFWGVAHKGLTNKQGRVAVKVPVAPADIPSP 518

RESULT 9

probable triacylglycerol lipase - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: Columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C:Accession: E71435
R:Bevan, M.; Bancroft, I.; Bent, B.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Emtian, K.D.; Kieger, M.; Schaefer, M.; Funk, B.
Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Prigodemenec
 erhot, A.; Moore, T.; Jones, J.D.G.; Eneva, T.; Palmer, K.; Benes, V.; Rehnman, S.; Anueva,
 C.; Chaitwalis, N.
 A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thaliana*
 A:Reference number: A71400; MUID:9812113; PMID:9461215
 A:Accession: E71435
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-601 <REV>
 A:Cross-references: UNIPROT:O23522; UNIPARC:UPI0000048570; GB:Z97342; NID:G2245031; PID:
 C:Genetics:
 A:Map position: 4COP9-4G3845

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Query March 18.6% Score 442.5; DB 2; Length 601;
Best Local Similarity 30.0%; Pred. No.2.6e-27;
Matches 128; Conservative 60; Mismatches 126; Indels 113; Gaps 14;

QY 11 SKPGTWPELLGSNMAAGLNPDLNDELRELLRCGDFCQVTDYTFINDONSSYCGSARYG 70
DB 125 SKLGSKMEELGLGNMAGLLDPLDENLRRELVYRGEEFVQALYHAFHSDPD---GSPRH- 179
QY 71 KADLLHTAPFGAGDRPDVAVYATATKVSYPEAFILKSREKX-----DRES 119
DB 180 -----VALPDGS--FRVYKSLYATSSVRLP-----KWIDVADLRLMTKQT 219
QY 120 NMIGYVAVSNDST- RVAGREVVYVMWGRCDRYEMVDVLAQOLSAHPILRTQOTTHVE 178
DB 220 SMVGVAACDDPREIRMGREIVIALRGTAFLLEW----- 255
QY 179 KVEHEBKSHKSSMYDCFINILGSAKMDKGKSDDDDDDDPKYMGCMITYTSEDPKS 238
DB 256 -SEN-----FRPNLV-SMPEPK--PDQSDPTPRPYKCEGFNSLYTTGQOHA 296
QY 239 PFTKLARSATOLQTKLKOILMTKYKQETLSITFAGHSIGATLSVSAFDIVENTLLEIPVA 298
DB 297 P-----SLAESLVGEISRLVELVYAGEBELISVTHSGIALAIALMLAADIDAEVPAHPVAV 352
QY 299 VVEGCEPKAGNKKFQOLPDSYPLNLAVLHYRNYIDLIPLYP----- 337
DB 353 FSGFGPRVGNREFADRLDLS-KGVKVLAVVNSQDVVTKVPGIFADNDKOGOSRNNGRSPGG 411
QY 338 -VKLM-----GYNIGIELEIDSRKSTFLDOSKNPSDMNLQAILHNVSGMHWKGEFK 390
DB 412 IMEWVERNNPWAYSHVGAELRVKDMKMSPLYLRPNMDVACCHDLDEAYLHLVDSGFSLNCPFR 471
QY 391 VVNRKSV 397
DB 472 ANAKRSL 478

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RESULT 10
H84723
probable triacylglycerol lipase [imported] - Arabidopsis thaliana
C|Species: Arabidopsis thaliana (mouse-ear cress)
C|Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jun-2004
C|Accession: H84723
R|Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Unayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, D.
Nature 402, 761-768, 1999
A|Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A|Reference number: A04420; MUID:20083487; PMID:10617197

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A:Accession: H84723
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-484 <STO>
 A:Cross-references: UNIPROT:Q9SIN9; UNIPARC:UPI00000485D3; GB:AE002093; NID:G4582461; PI
 C:Genetics:
 A:Gene: At2g31590
 A:Map position: 2

 Query Match 18.2%; Score 435; DB 2; Length 484;
 Best Local Similarity 27.8%; Pred. No. 7.7e-27;

	Matches	126; Conservative	74; Mismatches	134; Indels	120; Gaps	14;
QY	7	PLGLSKPSP-----	-----TWPELLGSNMAAGLLNPALNDBLRLLRLACGD	46		
Db	62	PVASSPPPIYCAFKPECCSGAATVPLSRWREIIOGNNMKDLIPLNPPLLOOEITRYGN	121			
QY	47	FCQVYVDFRINDONSSYCGSSRYGKADLLHKTFPGADRFEDVVAAYLTAKAVSPEAFL	106			
Db	122	LVSTCYKAFDLDPNRSKRYLNCCKYKQTLKETIDDEP-YQYTKYIYAT-----	POINT	175		
QY	107	LKSRSEKMDRESNMIGYVVSNDETSRAVGRREYVYVMGTCRDYEWVDVLAQLES-	165			
Db	176	NSPIQNEKNRRARPMGWVLAASDDSVKRLGRADIYVTFRGITVNPMLNFMSSLTIPAR	235			
QY	166	-HPLARTQOTTHVEKVENEEKSIHKSSWYDCNINILGASASDKKGSODDDDDPKYM	224			
Db	236	FHP-----HNPL-----	-----DKVYE	248		
QY	225	OGWMTIYTSDEDKSPETKLARSOTQKLQOMTKYKDETLSTTFAGHSIGATLSVVSAP	284			
Db	249	SGFLSLIYTSDESESKRGLESCROQLLSRILNNKTKGEESSITLLAGHSWSSLAQCLAY	308			
QY	285	DIVE-NLTT-----ELPYTAUVFGCKPKGNKKRQOLFDSYPNLVLHVRYVIDLIPLYP-	337			
Db	309	DIAELGLNRIKGDIPVTFVSFAGPRVGNLEPKKCEEL-GYKVLITVYNDVVTYKPG	367			
QY	338	-----VKLMG-----	YVNIIGIELEIDSRKSTFLKSDSKNPSDMHNLQALIHVS	380		
Db	368	VLFNENFRVLGGFYELPMWSCSCVYHVGVELTLD-----	FFDVQNISCVHDLQTYIDLLN	421		
QY	381	GHHGKYGKFKVYVKSIV-----ALVYKSCDPLK	408			
Db	422	Q-----RTNRSRVSDEDEDEDSDNVALLFELK	447			

RESULT 11
 E86192
 hypothetical protein [imported] - Arabidopsis thaliana
 C1Species: Arabidopsis thaliana (mouse-ear cress)
 C1Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C1Accession: E86192
 R1Theologos, A.; Ecker, J. R.; Palm, C. J.; Federspiel, N. A.; Kaul, S.; White, O.; Alonso, C.; Chiu, C. W.; Chung, M. K.; Conn, L.; Conway, A. B.; Conway, A. R.; Cressy, T. H.; Dewar, K.; Hansen, N. F.; Hughes, B.; Huizier, L.
 Nature 408, 816-820, 2000
 A1Authors: Hunter, J. L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J. H.; Li, Y.; Lin, X.; Liu, S. X.; Liu, Z. A.; Lueros, J. S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A1Authors: Salzberg, S. L.; Schwartz, J. R.; Shum, P.; Southwick, A. M.; Sun, H.; Tallon, B.; Ker, M.; Wu, D.; Yi, G.; Frazer, C. M.; Venter, J. C.; Davis, R. W.
 A1Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A1Reference number: AB6141; WUID:21016719; PMID:11130712
 A1Accession: E86192
 A1Status: preliminary
 A1Molecule type: DNA
 A1Residues: 1-471 <STO>
 A1Cross-references: UNIPROT:Q9MA46; UNIPARC:UPI000000A8FAC; GB:AE005172; NID:g66850308; PIR:G1Genetics:
 A1Map position: 1

	Query Match	17.3%	Score 412.5;	DB 2;	Length 471;
	Best Local Similarity	28.4%;	Pred. No. 4.7e-25;		
	Matches	123;	Mismatches 139;	Indels 99;	Gaps 11;
Qy	3 AEAQPLGSKPPTPELIGSNAMAGLLPNLNDELRELLRCGDFECVYDTFINDNSS	62			
Dd	73 AAATLPISR---WKEIQSNMWEVLIEPLSLTLOEITRYGNLSASTKGFPLNRSK	129			
Qy	63 YCGSSRYGADKLHHTKAFFPGADRFPVVAVLYLTATASYVEAEFLKRSRREKMDRESNMI	122			
Dd	130 RLTSCKYGGKNLLKSSEGI-HDPDGYOVTKTYIPTPINLNPIKNEPRAR-----WI	180			
Qy	123 GYVVVSNDETSVAGREVVYWRGTGRDYEWVDVIGAQLSAHPILRLTQOTTHVEKEN	182			

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Db 181 GYVAVSSDESIVKRLGRBDILVTFRGTVTNHEWMLANKSSLTPA----- 223
Qy 183 BEKSKHKSSWYDCFNINILGASAKDKGSGDDDDDDPKVMQGMNTIYTSDEKSPFTK 242
Db 224 -----RLDPNRPDPVKVSSGFLGLYTSSESKFGL 255
Qy 243 LSARTQTLKQLKQMTKYKDETLSTIFAGHSLGATLSVSAFDIVE---NLTFE---IPV 296
Db 256 ESCEQLLSLSRLMKNHKGSEISITLAGHSGSSSLAQDLAYDLAELGMQRREKVPV 315
Qy 297 TAVVFGCPKVGKPKFQQLFDSYPNLNLVLRNVNIDILPYVVKMG----- 342
Db 316 TVFSFAPGRVGNLGFKKRCEEL-GVKVLRITNVNDPIKFLGFLENFRSLGCVYELPW 374
Qy 343 -----YVNIETLEIDSKSTFLKSKSPSDMHNLOALIHVSGMHGK------GEF 389
Db 375 SCSCYTHVGVELTD-----FPVQNTSCVHDETYITTLVNRPRCSKLAVNEDNFGGEF 428
Qy 390 KVVNKRSAVALVVK 402
Db 429 --LNRITSELMFSK 439
```

RESULT 12

T01607

probable triacylglycerol lipase AC2944810 [Imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein F16B22.30; hypothetical protein T13E15.18

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 19-Feb-1999 #sequence revision 19-Feb-1999 #text_change 09-Jul-2004

C;Accession: T00412; T01607; A84883

R;Rounsfley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc

submitted to the EMBL Data Library, July 1997

A;Description: Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence.

A;Reference number: Z14146

A;Accession: T00412

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-357 <ROW>

A;Cross-references: UNIPROT:Q22170; UNIPARC:UPI0000048665; EMBL:AC002388; NID:g3420042;

A;Experimental source: cultivar Columbia

R;Rounsfley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,

submitted to the EMBL Data Library, July 1998

A;Description: Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence.

A;Reference number: Z14284

A;Accession: T01607

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-357 <ROW>

A;Cross-references: UNIPARC:UPI0000048665; EMBL:AC003672; NID:g3341671; PID:g3341700

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsfley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Wolfat, K.S.; Cronin, L.A.; Shen, M.; Yanke, S.E.; Unay, L.; Tallon, L.

euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84883

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-357 <STO>

A;Cross-references: UNIPARC:UPI0000048665; GB:AE002093; NID:g3344903; PID:AC31843.1; G

C;Genetics:

A;Gene: At2g44810; T13E15.18; F16B22.30

A;Map position: 2

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Query Match 16.9%; Score 404; DB 2; Length 357;
Best Local Similarity 29.6%; Pred. No. 1.5e-24;
Matches 124; Conservative 60; Mismatches 131; Indels 104; Gaps 15;
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Qy 19 ELGSMNAGLNPINDELRELLRLRCGDFCOVYTFINDONSYYCGSSRYGKADLHKT 78
Db 2 EYGGQNNDDGLDPLDDMLRREILRYGQFVESAYQAFDFDSSPYGTCTFRPSTILERS 61
```

```
Qy 79 AFGGADRFPDVAVLYATAKVSPPEAFLLKSRREKM-DRESNWIGVVVNSD--ETSRV 135
Db 62 GLRNSGYR--LTNLRATSGINLPR-WIEKAP--WMATQSSWIGVAVACODEEISRL 115
Qy 136 AGRREYVYVVRGCRDYEWDVYGAQLSNAHPLRLQOTTHVEKVENBEKSKSHKSWYD 195
Db 116 -GRDDVVISFRGATCTLEMLNLRATL-----THLPNGPT----- 149
Qy 196 CFNINILGASAKDKGSGDDDDDDPKVMQGMNTIYTSDEPKSPFTKLSARTQTLKQ 255
Db 150 --GANLNGNS-----GPNVESGFSLYTS-----GVHSLRDVREBIAR 187
Qy 256 LMTKYKDETLSTIFAGHSLGATLSVSAFDIVENTLTFVTAIVFGCPKVGKPKFQOL 315
Db 188 LIGSGDEPLSVTITGHSIGAATLAAVDIKTFPKKAPMVTAVISFGSPRGNRCFRKL 247
Qy 316 DSYPNLNLVLRNVNIDILPYLP-----YKMG-----YVNI 347
Db 248 EK-QGTVLRIVNSDDVITVYVGVLENREODNVTMTASIMPSNIOREVEETPMVYAEIG 306
Qy 348 IELEIDSKSTFLKSKSPSDMHNLOALIHVSGMHGKGFVKNKRSAVALVVKSGDF 406
Db 307 KEIQLSRSDSPHL-SLNVATCHELKYTLHLVDGF-----VSTCPF 347
```

RESULT 13

S76637

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S76637

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yaeuda

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

sp.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S76637

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-407 <KAN>

A;Cross-references: UNIPROT:Q55826; UNIPARC:UPI00000C0F74; EMBL:D64004; GB:AB001339; NID

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

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Query Match 6.8%; Score 162.5; DB 2; Length 407;
Best Local Similarity 20.7%; Pred. No. 3.8e-05;
Matches 82; Conservative 59; Mismatches 127; Indels 129; Gaps 15;
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Qy 19 ELGSMNAGLNPINDELRELLRLRCGDFCOVYTFINDONSYYCGSSRYGKADLHKT 78
Db 90 EINSVRLTPPLPYDRQISGLLRCSKIATQVLT--GKTIPYDGNIR-----QLP 140
Qy 79 AFGGADRFPDVV-----ALVATKAVSPPEAFLLKSR--REKMDRESNWIGVVVNS 128
Db 141 AYSDLDVEYQIASFRGRHAHISSEVAQIP-----LNTGDPDLKTDQEDSDSG----- 191
Qy 129 NDETSR-----VAGREYVYVVRGCRDYEWDVYGAQLSNAHPLRLQOTTHVEK 172
Db 192 --ETIRVVVVKVTOGIPVYLGITSSPRNLTVEFGTGTTEWVA-----NLBAQ 238
Qy 173 QTTVEKVENBEKSKHKSSWYDCFNINILGASAKDKGSGDDDDDDPKVMQGMNTIYT 232
Db 239 QIPTEKRSQGYFPKIH-----QGFIEHY- 262
Qy 233 SEDKSPFTKLSARTQTLKQMTKYKDETLSTIFAGHSLGATLSVSAFDI---VEN 289
Db 263 -----LRIVSPIPREIAOOLDPVAVCYVTGHSIGSLAVLALDAVLNLPN 308
Qy 290 LTTETPTAVAVFGCPKVGKPKFQQLFDSYPNLNLVLRNVNIDILPYLP--VKMGYNIG 347
Db 309 LRSDIOLYS--YACPRVGDVTFQOL-HSRQVPSYRIVNLADVILPLPTTGLGTGVHVG 365
```

QY 348 IELEIDSRKSTPLKDSKNPSDMNLQALIHVSGM 384
DB 366 QSMSPFSGSDILPN-----HVDITYQG 388

RESULT 14

T06657

hypothetical protein T6G15.100 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C/Accession: T06657

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X

submitted to the Protein Sequence Database, April 1999

A/Reference number: Z15791

A/Accession: T06657

A/Molecule type: DNA

A/Residues: 1-805 <BEV>

A/Cross-references: UNIPROT:Q9T0H5; UNIPARC:UPI000009C968; EMBL:AL049656; GSPDB:GN00062;

A/Experimental source: cultivar Columbia; BAC clone T6G15

C/Genetics:

A/Map position: 4

A/Intons: 89/3; 112/2; 135/3; 163/1; 193/3; 539/3; 560/3; 587/2; 625/2; 652/3; 690/3; 7

Query Match 5.5%; Score 131.5; DB 2; Length 805;

Best Local Similarity 22.2%; Pred. No. 0.03; Mismatches 101; Indels 105; Gaps 13;

Matches 73; Conservative 50; Mismatches 101; Indels 105; Gaps 13;

QY 96 TAKVPEAPFLKRSRKKMVDRESNMIGYVVSNDERSVAGREVVVWRGTCRDYEW 155

DB 378 TALAGTESGLATADTREADDEKED--GQVAINASKSLADMKNAQELLK-----QAD 429

QY 156 DIVGA--QLESAPLPLRTQOTTHVEKVENEEKSIHK---SNWDCFNILGASADKG 210

DB 430 NVGALMLVLAAYVP-----HLKSDVSGEKVIERKSSVTD---DVSGSSKTEKI 477

QY 211 KSGDDDDDDPKVMQGMNTIYTSDEP-----KSPFTKL----- 243

DB 478 SGLVNDGADKRAEEMKTLFSSNAESAMEAMALATLGHPSFKSEFEKLCLENDITD 537

QY 244 -----SARTQLTKLKQMLTKYKDET-----L 265

DB 538 TVQAVIRDARKRKVIAFRCTEQVHSGFLSAYDSVRIRIISLKMTIGYIDVTERDKM 597

QY 266 SITPAGHSGLATISVSAFIVENLTTE---IPYTAVFPCPKYGNKKFQOLF-----DS 317

DB 598 HVVVTGHSISGLGALATLALSLSSQLKRGATVTMTNFGSPRYGNKQFAEIVNQKVKDS 657

QY 318 YPNLNLVLRNVNIDLPYLPVKLMGYNI 346

DB 658 W-----RVNHRDIIPTVP-RIMGYCHV 679

RESULT 15

S64146

probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein G2842

C/Species: Saccharomyces cerevisiae

C/Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004

C/Accession: S64146; S71739

R:Sacribano, V.; Eraso, P.; Portillo, F.; Mazon, M.J.

submitted to the Protein Sequence Database, May 1996

A/Reference number: S64144

A/Accession: S64146

A/Molecule type: DNA

A/Residues: 1-1264 <ESG>

A/Cross-references: UNIPROT:P51125; UNIPARC:UPI0000052E2A; EMBL:Z72655; NTD:G132270; PI

R:Sacribano, V.; Eraso, P.; Portillo, F.; Mazon, M.J.

Yeast 12, 887-892, 1996

A/Title: Sequence analysis of a 14.6 kb DNA fragment of Saccharomyces cerevisiae chromos

A/Reference number: S71733; NUID:196437978; PMID:8840506

A/Accession: S71739

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-1264 <ESW>

A/Cross-references: UNIPARC:UPI0000052E2A; EMBL:X92670

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995

C/Genetics:

A/Gene: SGD:ITC1

A/Cross-references: SGD:S0003101

A/Map position: 7L

C/Keywords: transmembrane protein

F/549-565/Domain: transmembrane #status predicted <TM>

Query Match 5.1%; Score 121; DB 2; Length 1264;

Best Local Similarity 20.7%; Pred. No. 0.4; Mismatches 135; Indels 82; Gaps 14;

Matches 72; Conservative 58; Mismatches 135; Indels 82; Gaps 14;

QY 153 EWDVLAQLESAPLPLRTQOTTHVEKVENEEKSIHKSSWYDCFNILGASAS-----K 207

DB 262 EWPXDMKTKYKEDPPVVARNSANVSSPSEKMKRQSGSG-----KSNISNDASNKKETK 317

QY 208 DKGSGDDDDDDPKVMQGMNTIYTSDEPKSPPTKLSARTQLTKLKQMLTKYKDET-L-S 266

DB 318 KKKKPTFVNDSEN-----NSSEEDKKKQONTSETHSKRKKEANEETTERVES 367

QY 267 ITFAGHSGLATISVSAFIV-----ENLTIEIVTAVFPCPKYGNKKFQOLFDS-- 317

DB 368 VPTPANAEPQAVTITIMDLALPYQHPNIFPNLTYNEKLEICISGTYKLSRPFDSFG 427

QY 318 -----YPNLNLVLRNVNIDLP-----YPVLMG-----YVNI-----GIELIDSR 355

DB 428 KLIQAVPLNTFSGSKICLSHFSIDQFTISLKCDFELKGEVVLVNIROTSGEGLIENN 487

QY 356 -----KSTPLKDSKNPSDMNLQALIHVSGMVGKGEFVY-----NK 394

DB 488 GLPMKKKAETTTEDSENPSDMQNSFIRDMIKRSDKVEYKIVHDDPASDDILDNINH 547

QY 395 RSVLVNKKSCD-----FLKEE-----CLVPPAMVNVQKKGVNLKQGE 432

DB 548 NSGALLIEVFTALLRLFINEGDWSCIYVEN-WIIDDKGLMERKDE 593

Search completed: December 22, 2005, 19:47:51
Job time : 28.5 sec

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Query Match	55.0%;	Score 1311.5;	DB 2;	Length 412;
Best Local Similarity	56.0%;	Pred. No. 1.le-93;		
Matches 242;	Conservative 72;	Mismatches 91;	Indels 27;	Gaps 4;
16	TWPELLGSNAWAGLPLNDELRELLRCGDCFOVYDTTFINDONSSYCGSSRRYKADLL	75		

DR	Pfam: PF01764; Lipase_3; 1.	Score 1057; DB 2; Length 465
SQ	SEQUENCE 465 AA; 50453 MW; 5167A02D019FF0EE CRC64;	
Query Match		44.3%;
Best Local Similarity		46.8%; Pred. No. 9.5e-74;

Matches 206; Conservative 73; Mismatches 109; Indels 52; Gaps 6;

QY 11 SKGPTWPELGGNNAAGLNPDELRELLRCGDFCOVYTFINDONSSYCGSSRGX 70
 DB 17 SRP---WPELLGSAHMDGLDPLDLTRRLILCGDLCOVYTFINDONSSYCGSSRGX 73
 QY 71 KALLHKTAPGADRPDVAVLYATAKVSPPEAFLLKSRSEKMDRESNMIGYVAVNSD 130
 DB 74 RSTLLRTOFPAAGD--LSVAAYLYATSDATAFESMYSMSREMSKESNMIGYVAVNSD 132
 QY 131 ETSRVAGREVVYVWRCGTCDYEWVDVLAQLESAPHLRTQOTTHVEKVENEEKSIHK 190
 DB 133 AAAAAGGQRIYVYAMRGITISLEWVDVLAQLESAPHLRTQOTTHVEKVENEEKSIHK 169
 QY 191 SSYYDCENINLLGASAKDKGSDDDDDPKVMQGMNTIYTSDEPKSPFTKLSARTQ 250
 DB 170 -----ILPEGHGGRGRS-----RWKKGWVLYISYSDERSPEKTSARQOML 210
 QY 251 TKLKQMTKYKDETLSTTFAGSHLGATLSVVSAPDIYENLTTE-----IPVTAVVGCP 304
 DB 211 AAVRELAVARYANSLGVCVCGHSLGASLATLCAFDIYVNGSVKVGDAHLPVTAVVGSP 270
 QY 305 KVGKKFQOOLFDSYPNLNLVAVRNVDLPLYPVKLMGYVNIIGLEIDRSKSTFLDKSK 364
 DB 271 QIGNPEFKQFEBOPNLRALHVRNMPDLIPYEGILGYANVGKTLQVDSKSPYVRDT 330
 QY 365 NPSDMHNLOALHVVSGMHGVGFKVNVKRSVALVWNSCDFLKECLVPPAMVYVON 424
 DB 331 SPEDYHNLQGIILTVAGMNGKDEFLKQVRSVALVWNSGFLKSNLVPESSWVVERKNG 390
 QY 425 MVLNKGEMVLAPPEDEPTP 444
 DB 391 MVLGONGEMVLBPGEENLP 410

RESULT 4
 049523 ARATH
 ID 049523_ARATH PRELIMINARY; PRT; 419 AA.
 AC 049523;
 DT 01-JUN-1998 (TEMBLrel. 06, Created)
 DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
 DT 01-FEB-2005 (TEMBLrel. 29, Last annotation update)
 DE Lipase-like protein.
 GN Name=F28J12.210; Synonyms=Atg16550;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_Taxid=3702;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
 RA Bancroft I., Mewes H.W., Mayer K., Schueller C.;
 RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RA NUCLEOTIDE SEQUENCE.
 RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RA NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AL021710; CA16735.1; -; Genomic DNA.
 DR EMBL; AL161548; CAB78857.1; -; Genomic DNA.
 DR PIR; T04551; T04551.
 DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR InterPro; IPR002921; Lipase_3.

DR Pfam; PF01764; Lipase_3; 1.
 SQ SEQUENCE 419 AA; 47792 MW; 3B2B13089146482C CRC64;
 Query Match 33.1%; Score 789.5; DB 2; Length 419;
 Best Local Similarity 37.8%; Pred. No. 6.2e-53;
 Matches 169; Conservative 77; Mismatches 137; Indels 63; Gaps 8;

QY 17 WPELLGSAHMDGLDPLDLTRRLILCGDLCOVYTFINDONSSYCGSSRGXKADLLH 76
 DB 23 WRDLSCGNHKKMLQPLDQLREYIIHGYEMAQAGDTFINTESQAGASISRKDFFA 82
 QY 77 KT---AFPGADRPDVAVLYATAKVSPPEAFLLKSRSEKMDRESNMIGYVAVNSDET 132
 DB 83 KVGLEIAHP--YTKYKTKRIYATSDIHVESFLFPISREGMKSKESSNMIGYAVTDQ 140
 QY 133 SRVAGREVVYVWRCGTCDYEWVDVLAQLESAPHLRTQOTTHVEKVENEEKSIHK 192
 DB 141 TALLGRDIYVSRGVSQPLEWDEFEGLVNA----- 173
 QY 193 WYDCFNINLLGASAKDKGSDDDDDPKVMQGMNTIYTSDEPKSPFTKLSARTQ 252
 DB 174 -----IKIFG-----ERNDQVQIHQGMISITVSDERSPEFTTNARDVLR 215
 QY 253 LKQMTKYKDETLSTTFAGSHLGATLSVVSAPDIYENLTTE-----IPVTAVVGCP 304
 DB 216 VGRLEKYKDEVSITICGSLGALATLSTADIVANGVNRPKSRPKSCPVTAFVFPASP 275
 QY 305 KVGKKFQOOLFDSYPNLNLVAVRNVDLPLYPVKLMGYVNIIGLEIDRSKSTFLDKSK 364
 DB 276 RVGDSDFRKLFGSLIEDIRVLRNLPDVPVIRIP--IGYEVVDDEFIDRRKSPYMSPG 333
 QY 365 NPSDMHNLOALHVVSGMHGVGFKVNVKRSVALVWNSCDFLKECLVPPAMVYVON 422
 DB 334 NLATFHCLGTYLGVAGTQGTNKADLFRDVERAIGLVNKSVDGLKDECVNPKRVLKN 393

QY 423 KGMVNLKGEMVLAPPEDEPTPEFD 447
 DB 394 KGMVAQDDGSMELVDHEDNEDLD 418

RESULT 5
 09LNC2 ARATH
 ID 09LNC2_ARATH PRELIMINARY; PRT; 423 AA.
 AC 09LNC2;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Pp14.11 protein.
 GN Name=Pp14.11;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_Taxid=3702;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 RA Sakano H., Vaynsberg M., Lee J.M., Lenz C., Liu S.X., Pham P.,
 RA Toriumi M., Yu G., Chai C., Chio J., Choi E., Chung M., Gonzalez A.,
 RA Howing B., Liu A., Altafi H., Brooks S., Buehler E., Chao O., Conn L.,
 RA Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
 RA Miranda M., Nguyen M., Palm C.J., Shin P., Southwick A., Davis R.W.,
 RA Ecker J.R., Federapfel N.A., Theologis A.;
 RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AC025290; AAF80222.1; -; Genomic DNA.
 DR PIR; C86198; C86198.
 DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR InterPro; IPR002921; Lipase_3.
 DR InterPro; IPR008262; Lipase_AS.
 DR Pfam; PF01764; Lipase_3; 1.
 DR PROSITE; PS00120; LIPASE_SER; UNKNOWN 1.
 SQ SEQUENCE 423 AA; 48122 MW; E410984DC9F6DC74 CRC64;

DR GO:0006629; P:lipid metabolism; IEA.
 DR InterPro: IPR002921; Lipase_3.
 DR InterPro: IPR008262; Lipase_3.
 DR Pfam: PF01764; Lipase_3; 1.
 DR PROSITE: PS00120; LIPASE_SER; UNKNOWN 1.
 SQ SEQUENCE 411 AA; 45608 MW; 780C7A575A41959C CRC64;

Query Match 31.7%; Score 755.5; DB 2; Length 411;
 Best Local Similarity 37.4%; Pred. No. 2.7e-50;
 Matches 164; Conservative 65; Mismatches 150; Indels 59; Gaps 5;

QY 17 WPELLGSNAAGLNPINDELRELLRCGDFCQVYDPTINDQSSYCGSSRYGKADLLH 76
 DB 15 WREIHGSDMDGLDPDLDRRTVIRYGEWAQTYDAFNHEKLSRPAHSRFAARRFE 74
 QY 77 KTAFFPGADRFDDVAVLYATATKSVVPEAPFLKSRREKMDRESHWIGYVVSNDETS 136
 DB 75 RAQLPGHSAAYRVARFYATSCVAVPEPLILRSRRRCRESHWIGYVAVATDEGKAL 134
 QY 137 GRREVVYVWGTGCDYEWVDVLAQLESAPHLRTQOTTHVEKEVNEEKS IHKSSWYDC 196
 DB 135 GRDDIVAMGTQVQSLMIDMPVWPPKGLR----- 168
 QY 197 FNINLGASAKDKGSDDDDDDPKVMQGMWITYTSEDPKSPPTKLSARTQLOTKLKOL 256
 DB 169 -----DKASDAVHRGWLWYTSRDSSSHKKDSARDQVLSVAKL 209
 QY 257 MTKYKDELTSTPAGSLGATLSVSAFDIYEN-----LTTEIPTAVVFGCPKV 306
 DB 210 VSMYODELSITYVGHSLGALATLAFDIYENGYNAPRAAAAAGCPPTAFVAFASPRV 269
 QY 307 GNKKFQOLPDSYP--NNVNLVHRNVIDLPLVYKLMGVNIGLEIDSKSTFLDSK 364
 DB 270 GGGGFKRRFGAGRLGLRLRVNARADVPRP--PAPPHGVGTELLIDGESFYLRPG 328
 QY 365 NPSDMNHLQALHVVSGMHWK--GEFKVNVKRSVALVNSCDFLKEBCLVPPAMVYQNK 423
 DB 329 NELVNHLECYLHGAVAGAGGEGFRLAVERDVALANKSYGALRDHVAIPAGWIMDSNR 388
 QY 424 GMYLNDGEMVLAPEED 441
 DB 389 GMYRGADGRWTLMDRED 406

RESULT 8

Q6F357_ORYSA PRELIMINARY; PRT; 407 AA.

AC Q6F357;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Putative lipase.
 GN Name=OJ1268_B08.4; Synonym=OJ1735_C10.22;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Chow T.-Y., Hsiang Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-Y., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Lwu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.,
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

RP NUCLEOTIDE SEQUENCE.
 RA Chow T.-Y., Hsiang Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-Y., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Lwu H.-L.,

RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-M., Yu C.-Y., Yu S.-M.,
 RA Wu H.-P., Shaw J.-F.,
 RT "Oryza sativa BAC OJ1735_C10 genomic sequence."
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC104284; AAU4411.1; -, Genomic DNA.
 DR EMBL: AC098832; AAT69581.1; -, Genomic DNA.
 DR Gramene: Q6F357;
 DR GO:0004806; F:triacylglycerol lipase activity; IEA.
 DR GO:0006629; P:lipid metabolism; IEA.
 DR InterPro: IPR002921; Lipase_3.
 DR InterPro: IPR008262; Lipase_AS.
 DR Pfam: PF01764; Lipase_3; 1.
 DR PROSITE: PS00120; LIPASE_SER; UNKNOWN 1.
 SQ SEQUENCE 407 AA; 43766 MW; F0FC2359EF0B4888 CRC64;

Query Match 31.0%; Score 740.5; DB 2; Length 407;
 Best Local Similarity 37.5%; Pred. No. 4e-49;
 Matches 163; Conservative 70; Mismatches 139; Indels 63; Gaps 7;

QY 17 WPELLGSNAAGLNPINDELRELLRCGDFCQVYDPTINDQSSYCGSSRYGKADLLH 76
 DB 14 WREIHGSDSMGGLDPDLDRSILSYGELVQATYDFNRERSRPAAGACVGHGDL- 72
 QY 77 KTAFFPGADRFDDVAVLYATATKSVVPEAPFL--LKSRREKMDRESHWIGYVVSNDETS 133
 DB 73 AAAGASAGSYATKFFVATSGLPVPEAFLLPLPLPSPAMSRSHNMGVAVATDEGV 132
 QY 134 RVAGREVVYVWGTGCDYEWVDVLAQLESAPHLRTQOTTHVEKEVNEEKS IHKSSW 193
 DB 133 AALGRDVIAMGTQVQSLMIDMPVWDFPTVPAPV----- 166
 QY 194 YDGFNINLGASAKDKGSDDDDDDPK--VMQGMWITYTSEDPKSPPTKLSARTQLOT 251
 DB 167 -----VLGAAA-----ANPRAIVHRGFLSVTSSKSKYKASARDQVLE 208
 QY 252 KLQMLTKYKDELTSTPAGSLGATLSVSAFDIYEN-----LTTEIPTAVV 300
 DB 209 EVRIMELYKDEVTSLVGHSLGALATLNAVIVANGANCPSASSSQPCPTVAIV 268
 QY 301 FGCPKVGNNKFFQOLPDSYPNLVNLVHRNVIDLPLVYKLMGVNIGLEIDSKSTFL 360
 DB 269 FASPRVGDGFFKAFAFSPDLRLHVNAGDVEMVPP--LGYADVAVKLRISTRSPYL 326
 QY 361 KDSKNPDMNHLQALHVVSGMHWKGEFKVNVKRSVALVNSCDFLKEBCLVPPAMVY 420
 DB 327 RSPGTTETLHNECYLHGAVAGGEGAGFRLAVERDVALANKGYDALKQTPPEPRMVS 386
 QY 421 QNKGMYLNDGEMVLA 435
 DB 387 KNRCMYVDADGHMAL 401

RESULT 9

Q6RZ40_ORYSA PRELIMINARY; PRT; 420 AA.

AC Q6RZ40;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Lipase-like.
 GN Name=OJ159_D09.27;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanihara H.,
 RA Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi H.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijiwhita S., Honda M., Ichikawa Y., Ikonuma A., Iijima M., Ikeda M.,

RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machida K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1.";
 RL Nature 420:312-316(2002).
 DR EMBL; AP003792; BAB89211.1; -; Genomic_DNA.
 DR Gramene; Q8R240; -;
 DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR InterPro; IPR002921; Lipase_3.
 DR InterPro; IPR008262; Lipase_AS.
 DR Pfam; PF01764; Lipase_3; 1.
 DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
 DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
 SQ SEQUENCE 420 AA; 45328 MW; 5915CC680F5F2A0 CRC64;

Query Match 30.9%; Score 736; DB 2; Length 420;
 Best Local Similarity 37.5%; Pred. No. 9,3e-49;
 Matches 162; Conservative 69; Mismatches 141; Indels 60; Gaps 9;
 QY 22 GSNAMAGLNPINDELRELLRCGDFCQVYDTFINDNSSYCGSSRYKADLHKTAFP 81
 DB 31 GKMDMDGLDLPDLDRDITRIGELAOATSDALIGDPASFPAGASRAAPAFILKRA-A 89
 QY 82 GGADRFDVAVLYATKAVSPEAFLLK--SSREKMDRESNMGVGVVNSDSTSVAGRR 139
 DB 90 SDPARYVTRFVYATSSVRLPDAFWPRAPASGAAMSGESNMGVVAADGVAAKAGRR 149
 QY 140 EYVYVWRTGCTDYENVVLGAQLBSAHLRTQCTTHVEKENBEKSIHKSMTDCNI 199
 DB 150 DIVVAMRGTKRAVEWANDLITLVADGVV----- 179
 QY 200 NLDSASKDKGSGDDDDDDPKVMQGMWITYTSEDPKSPFTKLSARTQLTKLQKOLMTK 259
 DB 180 -----GPRPGW-----TQPSVHKGFLSVYTSKSPSSPKLSARQVLAETRLIRA 226
 QY 260 YKDETLSTFAGHSIGATLSVSAFDIVEN-----LTTEIPYTAVVFGCPKYGNKKFQ 312
 DB 227 YKNEKSTITIGHSIGALSTLNAIDIVANGVWGSRRVPYVLAIALASPRVDDQFK 286
 QY 313 QLPFSYPLNVLHVRNVLDLP-LYPVLMGVNIGILELDSKSTFLKSKSPSDMHN 371
 DB 287 RAFSTSTNLSLRVANNADIVFTILPSAF--FKDVGAELVDTRRSPYLKDPAGPAQWNN 344
 QY 372 LQALIHVVGSMHGVGE---FKVNVKRSVALVNSCDFLKEECVLPAMWVYONKQWYLN 428
 DB 345 LECTYHAAVAGTGA-GDGAQFSLVVDRLDALVKNKVDLRLDEYQVPAAMWVEKKMGWYON 403
 QY 429 KDGWVLAPEE 440
 DB 404 ASGRWVLQDHEE 415

RESULT 10
 OSVP27 ORYSA PRELIMINARY; PRT; 418 AA.
 AC OSVP27
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE Lipase-like protein.
 GN Name=OJ1159 D09.22;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Maekawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijioka S., Honda M., Ichioka Y., Idonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machida K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1.";
 RL Nature 420:312-316(2002).
 CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2O) = diacylglycerol + a
 carboxylate.
 DR EMBL; AP003792; BAB89211.1; -; Genomic_DNA.
 DR Gramene; OSVP27; -;
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
 DR GO; GO:0016042; P:lipid catabolism; IEA.
 DR InterPro; IPR002921; Lipase_3.
 DR InterPro; IPR008262; Lipase_AS.
 DR Pfam; PF01764; Lipase_3; 1.
 DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
 KW Hydroxylase; Lipid degradation.
 SQ SEQUENCE 418 AA; 46822 MW; D484B9A38F9A6285 CRC64;

Query Match 30.6%; Score 730; DB 2; Length 418;
 Best Local Similarity 38.2%; Pred. No. 2,7e-48;
 Matches 175; Conservative 51; Mismatches 156; Indels 74; Gaps 6;
 QY 17 WPELSSNAMAGLNPINDELRELLRCGDFCQVYDTFINDNSSYCGSSRYKADLHK 76
 DB 5 WRELHSGHMDGLDLPDLRLRCLITYGEMIMATYEAFIGEHSPPNAGACRYHADLFR 64
 QY 77 K--TAIFGADRPRVAVLYATKAVSPEAFLLKSRREKMDRESNMGVGVVNSDSTSR 134
 DB 65 RVDVSHRPGW--YAATRYIYATANADVHGVLLRLCRBGRATECNMGVVAATDGAAL 121
 QY 135 VAGREVVYVWRTGCTDYENVVLGAQLBSAHLRTQCTTHVEKENBEKSIHKSMT 194
 DB 122 ALGRDVLVAKRGTORALEWADLKLAPASAGL----- 156
 QY 195 DCFNINILGSASKDKGSGDDDDDDPKVMQGMWITYTSEDPKSPFTKLSARTQ----- 248
 DB 157 -----GREGADGTDPVHGRGYLSYTSSEDPQSELNKGSHRMQNKLLGF 199
 QY 249 -----LOTKLQKOLMTKYKDETLSTFAGHSIGATLSVSAFDIVEN----- 290
 DB 200 DPMKQTLKQVLTETARLMDKXKBETSIYVIGSLGATLTLNADIAANSYNTSSLSPS 259
 QY 291 -TTEIPYTAVVFGCPKYGNKKFQQLFDSYPLNVLHVRNVLDLP-LYPVLMGVNIGILE 349
 DB 260 GETRAPYTAVVFGSPRGDGRFRAFRRLRLRLRANRPDRIPHP--VGADVGVE 317
 QY 350 LEIDSRKSTFLKSKSPSDMHNLAALHVVSGMHGVGEFKVNVKRSVALVNSCDFLKE 409
 DB 318 LLITRLSPFLRRGSSSQSHDECHLHGVAGHGDHGRGFEVLVVDRLVALVNFDDCLAD 377
 QY 410 ECLVPLAMWVYONKQWYLNKDGWVLAPEEDPPEED 447
 DB 378 EYVYVWRTGCTDYENVVLGAQLBSAHLRTQCTTHVEKENBEKSIHKSMTDCNI 415

RESULT 11
 OSVP27 ARATH PRELIMINARY; PRT; 527 AA.
 AC OSVP27
 DT 09-08-2005 (ARATH)
 ID OSVP27 ARATH PRELIMINARY;
 RN [1]

DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
 DE Hypothetical protein F5D21.19 (A1951440/F5D21_19).
 GN Name=F5D21.19;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Uteback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Town C.D., Kaul S.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamita A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Phan P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Kim C.J., Chen H., Cheuk R., Shin P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Hsuan V.W., Ishida J., Jones T., Kamita A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S.C., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 CC carboxylate.
 CC EMBL: AC024261; AAC52635.1; -; Genomic_DNA.
 DR EMBL: AF424572; AL01366.1; -; mRNA.
 DR EMBL: AY142023; AA098287.1; -; mRNA.
 DR PIR: F96552; F96552.
 DR GO: GO:0016787; F:triacylglycerol lipase activity; IEA.
 DR GO: GO:0016042; P:lipid catabolism; IEA.
 DR GO: GO:0016042; P:lipid catabolism; IEA.
 DR InterPro: IPR002921; Lipase_3.
 DR InterPro: IPR008262; Lipase_AS.
 DR InterPro: IPR003379; Ser_estra.
 DR Pfam: PF01764; Lipase_3; 1.
 DR PROSITE: PS00120; LIPASE_SER; UNKNOWN 1.
 KW Hydrolyase; Hypothetical protein; Lipid degradation.
 SQ SEQUENCE 527 AA; 60321 MW; 2161452f6c7f1a92 CkC64;

Query Match 29.5%; Score 703.5; DB 2; Length 527;
 Best Local Similarity 35.5%; Pred. No. 4.4e-46;
 Matches 169; Conservative 69; Mismatches 133; Indels 103; Gaps 14;

QY 17 WPBLSSNANAGLNPINDELRLRLRCGDFQVYTFINDONSSYCGSSRYKADL-- 74
 DB 91 WREVOGQNMWEGQIDPMMNHLRLRIIRYGEPAQACYSFDFPSKTKYCGSCYHPSDFPL 150
 QY 75 -----LHKTAFPGADPFDDVAVLYATAKVSPFAFLKSRKMRKMPRESMIGYVAVSN 129
 DB 151 NLDLHLK-----GTTIRYLYATSNILP-EPKQGLSSISWCHAMWGFVAVAT 201
 QY 130 D--ETSVAGREYVYVWVGTGRDYEWVDVLAOLDSAPLRLTQOTTHVEKVENEEKS 187
 DB 202 DEEVVSL-GRDVIAMRGVTYLVEMT----- 228

QY 188 IHKSWYDFCNINMLGSASXDKGSDDDDDPKVMQGMWITITSEDPKSPFTLSART 247
 DB 229 -----YDL-----KDLCSANFGDDPSIKELGHNLDLYTKKEDCKSPFSFAR 272
 QY 248 QLOTKLQMLTKRYKDE---TLSTFAGHSLGATLVSVASFDIVE-NL-----TTEIPV 296
 DB 273 QVLAEVKRLIEYVOTESEGHKTSITVGHSLGASLALVSAVDIAELMLNHPENNYKPI 332
 QY 297 TAVFGCPKYGKKFQQLFPSYPLNVLHVRNYVDLIPLYVKL----- 340
 DB 333 TVSFSGPGRVGNLRFKRCDEL-GVKVLRVNVDKVPVPGVFTNEKFPQKVEEKTS 391
 QY 341 --NGYVIGIEIRIDSKSTFLKDSKPSDMMQATLHVSGWGVKGS-----FKYVVK 394
 DB 392 PPMSTAVHGVLELADHKKSFFLKTQOLGCANLEALHVDYGHGDEBAKGFCLVTK 451
 QY 395 RSVALVVKSCDPLKECLVPPAMVWVQNKGMVNLKDEWYL--APPEEDPTPE 445
 DB 452 RDLALVVKSCDPLRGEYHVPFCWRQDENKGMVVKVGDGQWTLPRDLLEPHGPE 504

RESULT 12
 ID 004340 ARATH PRELIMINARY; PRT; 529 AA.
 AC 004340
 DT 01-JUN-1997 (TReMBLrel. 04, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
 DE Putative lipase.
 GN Name=At2G30550;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Town C.D., Haas B.J., Wu D., Maiti R., Hannick L.I., Chan A.P.,
 RA Tallon L.J., Rooney T., Uteback T.R., Vanaken S.E., Feldblum T.V.,
 RA White O., Fraser C.M.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Town C.D., Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=2208475; PubMed=12093376;
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamita A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shin P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [1]
 NCLECTOTIDE SEQUENCE.
 RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hsuan V.M.,
 RA Lee J.M., Quach H.L., Tang C., Toriumi M., Wallender E.K., Wong C.,
 RA Wu H.C., Yu G., Carninci P., Chen H., Cheuk R.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamitani A., Kawai J., Kim C.J.,
 RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
 RA Shim P., Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W.,
 RA Ecker J.R., Theologis A., Trimp M.G., Wu T., Shinozaki K., Davis R.W.,
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
 CC carboxylate.
 DR EMBL: U93215; AAB63082.2; -; Genomic_DNA.
 DR EMBL: AY086021; AAM63231.1; -; mRNA.
 DR EMBL: AY091143; AAM14092.1; -; mRNA.
 DR EMBL: AY142594; AAN13163.1; -; mRNA.
 DR PIR: G84709; G84709.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0004806; F:triacylglycerol lipase activity; IEA.
 DR GO: GO:0016042; P:lipid catabolism; IEA.
 DR InterPro: IPR002921; Lipase_3.
 DR InterPro: IPR008262; Lipase_AS.
 DR InterPro: IPR00379; Ser_estrs.
 DR Pfam: PF01764; Lipase_3; 1.
 DR PROSITE: PS00120; LIPASE_SER; UNKNOWN_1.
 DR HydroLase; Lipid degradation.
 KM SEQUENCE 529 AA; 60402 MW; 2F02B3C51953B020 CRC64;
 SQ
 Query Match 28.8%; Score 686.5; DB 2; Length 529;
 Best Local Similarity 35.6%; Pred. No. 9.4e-45;
 Matches 160; Conservative 78; Mismatches 133; Indels 79; Gaps 14;
 QY 16 TWPELLGSNMAAGLNPINDELRELRLRCGFCQVTVTFINDNSSYCGSSRYGKADLL 75
 DB 104 TWKRIQGBDDWAGLMDPMDPLRLSELRLRYGEMAQCYDAFDPDPASKYCGTSKRTREFF 163
 QY 76 HKTAFPGGADR-FDVVAIYATATKAVSVEAFILKRSREKMDRESNMGVYVNSDSTR 134
 DB 164 DSL---GMIDSGEVARLYATSNINLPN-FPSKSRMSKWSKANNMGYAVASDDSTR 219
 QY 135 -VAGREVVYVWRCGRDYENVVYGAQLSAPHLLRTQOTTHVEKVENEEKSIHKSWS 193
 DB 220 NRLGRDIALAMRGVTLEWIALDKYLKPV-----TENKIR----- 257
 QY 194 YDCFNINILGSASDKGSGDDDDDDPKVMQGMWTIYTSDEPKSPFTKLSARTQLOTKL 253
 DB 258 -C-----PDPAVKESGFLDLYTDKOTTCFKAFSAREQILTEV 295
 QY 254 KQMTKYKD---TLSTFAGHSIGATLSVVSADPIVE---NLTE---IPVTAVFGCP 304
 DB 296 KRLVBEHDDDDSDSLITVTHSGLSGALAILSAVYIAEMRLNRSKGVIPVTAVLYGCP 355
 QY 305 KVGKKFQQLFDSYFNINLVHVRVYDILPLYPVKMG-----YVNI 347
 DB 356 RVGVNRFERMEEL-GVAVRVVNVHADVPKSPGFLINESRPHALMKIAEGLPMCYSHVG 414
 QY 348 IELIDSKSTFLDKSKNPSDMHNLQALIHVSGMHGKGE-FKVNKRVSVALVYKSCDF 406
 DB 415 BELALDHQNSPFLKPSVSTAHNLAMHLIDYHG-KGERFVLVSGRDHALVYKASDF 473
 QY 407 LKEECLVPAMVWVONKGMVINKGDEWYLA 436
 DB 474 LKEHQLIPFMRQDANKGMVNSSEGRWIOA 503
 RESULT 13
 Q9M9Y7_ARATH PRELIMINARY; PRT; 515 AA.
 AC Q9M9Y7_ARATH PRELIMINARY; PRT; 515 AA.
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)

DE FAH5.11 protein (lipase, putative).
 GN Name=FAH5.11; Synonym=Atg106800;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eustosida II; Brassicales; Brassicaceae; Arabidopsie.
 OC NCBI_TaxID=3702;
 RN [1]
 NCLECTOTIDE SEQUENCE.
 RA Federepiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Aliafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremetzkala I., Kim C., Lenz C., Li J., Liu S.,
 RA Luros S., Schwartz J., Shim P., Toriumi M., Vysatekale V.S.,
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.,
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 NCLECTOTIDE SEQUENCE.
 RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
 RA Palm C.J., Bower L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamitani A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.,
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
 CC carboxylate.
 DR EMBL: AC011001; AAF63138.1; -; Genomic_DNA.
 DR EMBL: AY095599; AAM20450.1; -; mRNA.
 DR PIR: H86202; H86202.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0004806; F:triacylglycerol lipase activity; IEA.
 DR GO: GO:0016042; P:lipid catabolism; IEA.
 DR InterPro: IPR002921; Lipase_3.
 DR InterPro: IPR008262; Lipase_AS.
 DR InterPro: IPR00379; Ser_estrs.
 DR Pfam: PF01764; Lipase_3; 1.
 DR PROSITE: PS00120; LIPASE_SER; UNKNOWN_1.
 DR HydroLase; Lipid degradation.
 KM SEQUENCE 515 AA; 58445 MW; DD59442CB9166451 CRC64;
 SQ
 Query Match 28.1%; Score 670; DB 2; Length 515;
 Best Local Similarity 35.1%; Pred. No. 1.7e-43;
 Matches 157; Conservative 73; Mismatches 111; Indels 76; Gaps 12;
 QY 16 TWPELLGSNMAAGLNPINDELRELRLRCGFCQVTVTFINDNSSYCGSSRYGKADLL 75
 DB 88 TWKRIQGBDDWAGLMDPMDPLRLSELRLRYGEMAQCYDAFDPDPASKYCGTSKRTREFF 147
 QY 76 HKTAFPGGADR-FDVVAIYATATKAVSVEAFILKRSREKMDRESNMGVYVNSDSTR 134
 DB 148 DSLGIIDSG--YEVARLYATSNINLPN-FPSKSRMSKWSKANNMGYAVASDDSTR 204
 QY 135 V-AGREVVYVWRCGRDYENVVYGAQLSAPHLLRTQOTTHVEKVENEEKSIHKSWS 193
 DB 205 CRLGRDIALAMRGVTLEWIALDKYLKPV-----SGNG 240
 QY 205 CRLGRDIALAMRGVTLEWIALDKYLKPV-----SGNG 240
 DB 241 FRC-----PDPAVKESGFLDLYTDKOTTCFKAFSAREQILTEV 280
 QY 254 KQMTKYKD---EFLSTFAGHSIGATLSVVSADPIVE---NLTE---IPVTAVFGCP 304
 DB 281 KRLVERGEDEGELSLITVTHSGLSGALAVLSAVYIAEMRVNRSKGVIPVTAVLYGCP 340
 QY 305 KVGKKFQQLFDSYFNINLVHVRVYDILPLYPVKMG-----VYKMG-----YVNI 347
 DB 341 RVGVNRFERMEEL-GVAVRVVNVHADVPKSPGFLINESRPHALMKIAEGLPMCYSHVG 399
 QY 348 IELIDSKSTFLDKSKNPSDMHNLQALIHVSGMHGKGE-FKVNKRVSVALVYKSCDF 407
 DB 400 EMLLDHQSFPFLKPSVSTAHNLAMHLIDYHGKGRFVLVSGRDHALVYKASDF 459
 QY 408 KEECLVPAMVWVONKGMVINKGDEWYLA 434

Db 460 KDHFMVPPYWRQDANKGVNRTDGRW1 466

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RESULT 14
082274 ARATH PRELIMINARY; PRT; 355 AA.
ID 082274
AC 082274
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Putative lipase.
GN Name=At2g31100;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Romling C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005311; AAC63840.1; -; Genomic_DNA.
DR PIR; E84716; E84716.
DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
DR GO; GO:0006629; P:lipid metabolism; IEA.
DR InterPro; IPR002921; Lipase_3.
DR InterPro; IPR008262; Lipase_AS.
DR Pfam; PF01764; Lipase_3; 1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
SQ SEQUENCE 355 AA; 40471 MW; 18CE5655DFCE4C7 CRC64;

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Query Match 25.8%; Score 616; DB 2; Length 355;
 Best Local Similarity 32.9%; Pred. No. 1.7e-39;
 Matches 146; Conservative 69; Mismatches 111; Indels 118; Gaps 8;

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QY 17 WPELISNAAGLNPINDELRELLRCGDFCQYTYDTFINDONSSYCGSSRYGKADLLH 76
DB 9 WKELSSSKKKDLDPIDLRKYLTHYGDAEEL-----AATPKSSLE 54
QY 77 KTAPEGADRDVAVYIATKAVSVEPAFLKSRREKMDRESNMIGYVVSNDTSRA 136
DB 55 P-----VTSKPTL-----SDEGKLL 70
QY 137 GREVVYVWRGTCRDYEMVDVIGAOESAHRLATQOTTHVEKENEKKS IHKSSWYDC 196
DB 71 GRKGVVAMRGTTQLYEMADDFPLESA----- 99
QY 197 FNILLSASKDKGSDDDDDPKYMGWMTIYSEDPSPTKLARTQOTKLKOL 256
DB 100 --VWFFGCA-----NNDPRVANGTSLSTIDPSRFDKTSAGQVQVBEKRL 147
QY 257 MTKYKDETLITFAGSLGATLSVSAFDIVEN-----LTTEIPYAVVFCPCRYGN 308
DB 148 LELYKNEDVTITLGHSLGAVMSITLSAADFLHNMKPTKPSLQHSLSCTVAPAFSGPQIGD 207
QY 309 KKQQQLFDSYPNLVNLAHVNVYIDILPLYPVGLMKYVNIIGLELSDSKSTLKSKPSD 368
DB 208 RSPFRVLESLEHLHILVTVNPDLIPRPV--FRFTDIGELQINTLKSEYLSKSLNGH 265
QY 369 WHNLQALIHVVGSHGVGKFEKVVNKRVALVNSCDFLKEECVPPAMVWQKGVNLN 428
DB 266 FHNLEALIHGVAGTQHNQGEFKLEINDIALVNGGLALBCKYLVPGHMVLEKKNVQS 325
QY 429 KDGSEVLT-----APPEEDPTPE 445
DB 326 DDGTWKLNGDRSKKKQGEDEKEE 349

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RESULT 15
09C8G6 ARATH PRELIMINARY; PRT; 529 AA.
ID 09C8G6
AC 09C8G6
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Lipase, putative.
GN Name=TK22.3;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
RA Maiti R., Romling C.M., Koo H., Fujii C.Y., Utecherback T.R.,
RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2O) = diacylglycerol + a
CC carboxylate.
DR EMBL; AC025295; AAC51101.1; -; Genomic_DNA.
DR PIR; A86428; A86428.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004806; F:triacylglycerol lipase activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR002921; Lipase_3.
DR InterPro; IPR008262; Lipase_3.
DR InterPro; IPR000379; Ser_eatrs.
DR Pfam; PF01764; Lipase_3; 1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW Hydrolyase; lipid degradation.
SQ SEQUENCE 529 AA; 60742 MW; BA21D67856CD097E CRC64;

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Query Match 25.4%; Score 606.5; DB 2; Length 529;
 Best Local Similarity 32.0%; Pred. No. 1.6e-38;
 Matches 151; Conservative 79; Mismatches 157; Indels 85; Gaps 15;

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QY 1 MAEAOPLGSKGCPTEPELLGSNAAGLNPINDELRELLRCGDFCQYTYDTFINDON 60
DB 104 MTPAASP--REKISKWRRLHGSNNMENLDPILPMLRREVTXKGFEVESYDSDLPDL 161
QY 61 SSYCGSSRYGKADLLHKTAFPGADR--FDVAVLYATKAVSVEPAFLKSRREKMDRE 118
DB 162 SEFGSSRYNRNKLFEEL---GLTRHGYVTYKIYMSRVDPQW--LSALGETWSKD 216
QY 119 SNMIGYVVSNDTSRYVAGREVVYVWRGTCRDYEMVDVIGAOESAHPLRLTQOTTHVE 178
DB 217 SNMNGFVAVAGDRESLHIGRDIYAVRGTVTFEMFMDLRTSMEP----- 262
QY 179 KVNEEKKS IHKSSWYDCFNINLGSASKGKSDDDDDDPKYMGMWMTIYSEDPS 238
DB 263 -----FDC-----EGK---HGKTVVVGSGFLSYNSKSELT 291
QY 239 PFTKLARTQOTKLKOLMTKYD--ETLSITFAGSLGATLSVSAFDIVENLTTEIP- 295
DB 292 RINKESASEQTMDEBKLVNPFQDGEVSLITTHGSLGALALMAYEAR---DVFA 347
QY 296 ---VTAVFECPCRYGNKKFQQLFDSYPNLVNLAHVNVYIDILPLYP---VKLMG----- 342
DB 348 LSGNISVTSFGADRVGLAFKELNSL--GVKVLRVVVKQDIPVLPGLIVENKVLNKLNPI 406
QY 343 -----YVNIIGLELSDSKSTFLKDSKNPSDMHNLQALIHVVGSHGVGKFEKVVNKR 395
DB 407 TSLRNWYLRHVGTQLKLDVSSPYVKRSDLGRAHNLLEVYLHVLVDGPHRRKSSGFRVAVAR 466
QY 396 SVALVNSCDFLKEECVPPAMVWQKGVNLND--GEVY--LAPPEEDPTPE 444

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Db 467 DVASVVKSTMDLIDLRLIPFPMYQVAHKGLITKQGRWVXVRAPEDIPSP 518

Search completed: December 22, 2005, 19:42:26
Job time : 151.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 22, 2005, 19:42:37 ; Search time 8 Seconds

(without alignments)
398.546 Million cell updates/sec

Title: US-10-674-540A-2

Perfect score: 2385
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 54001 seqs, 7132810 residues

Total number of hits satisfying chosen parameters: 54001

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:
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2: /cgn2_6/ptodaca/1/pubpaa/US06_NEM_PUB pep:*
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8: /cgn2_6/ptodaca/1/pubpaa/US00_NEM_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128.5	5.4	267	6	US-10-495-597-5 Sequence 5, Appli
2	116	4.9	278	6	US-10-495-587-9 Sequence 9, Appli
3	115.5	4.8	270	6	US-10-495-587-11 Sequence 11, Appli
4	110.5	4.6	269	6	US-10-495-597-14 Sequence 14, Appli
5	108	4.5	270	6	US-10-495-597-12 Sequence 12, Appli
6	101.5	4.3	270	6	US-10-495-597-4 Sequence 4, Appli
7	98	4.1	269	6	US-10-495-597-13 Sequence 13, Appli
8	97.5	4.1	265	6	US-10-495-587-11 Sequence 1, Appli
9	97	4.1	312	6	US-10-495-587-6 Sequence 6, Appli
10	94	3.9	4128	6	US-10-770-726-77 Sequence 77, Appli
11	91.5	3.8	264	6	US-10-495-597-2 Sequence 2, Appli
12	89.5	3.8	269	6	US-10-495-597-3 Sequence 3, Appli
13	87.5	3.7	478	6	US-10-131-826A-138 Sequence 138, App
14	87.5	3.7	478	7	US-11-174-150-27 Sequence 27, Appli
15	87	3.6	278	6	US-10-495-587-10 Sequence 10, Appli
16	87	3.6	1933	6	US-10-523-912-2 Sequence 2, Appli
17	85.5	3.6	803	6	US-10-821-234-1643 Sequence 1643, Ap
18	85	3.6	274	6	US-10-495-597-7 Sequence 7, Appli
19	85	3.6	1067	7	US-11/062 Sequence 3, Appli
20	85	3.6	1092	7	US-11/062 Sequence 6, Appli
21	84	3.5	539	6	US-10-467-657-3870 Sequence 3870, Ap
22	84	3.5	799	7	US-11-074-176-348 Sequence 348, App
23	84	3.5	805	7	US-11-074-176-172 Sequence 172, Appli
24	80.5	3.4	1087	7	US-11-117-169-10 Sequence 10, Appli
25	79.5	3.3	390	6	US-10-485-517-235 Sequence 235, App

26	79.5	3.3	805	6	US-10-485-517-198 Sequence 198, App
27	79.5	3.3	1020	6	US-10-513-786-4 Sequence 4, Appli
28	79.5	3.3	1900	6	US-10-513-786-3 Sequence 3, Appli
29	79.5	3.3	3704	6	US-10-513-786-1 Sequence 1, Appli
30	78.5	3.3	710	6	US-10-467-657-4292 Sequence 4292, Ap
31	78	3.3	627	6	US-10-873-528-191 Sequence 191, App
32	77.5	3.2	419	7	US-11-084-624-18 Sequence 18, Appli
33	77.5	3.2	999	6	US-10-793-626-2594 Sequence 2594, Ap
34	77	3.2	348	7	US-11-129-143-72 Sequence 72, Appli
35	76	3.2	447	6	US-10-632-150-10 Sequence 10, Appli
36	76	3.2	447	7	US-11-073-457-10 Sequence 10, Appli
37	76	3.2	447	7	US-11-073-460-10 Sequence 10, Appli
38	76	3.2	477	6	US-10-131-826A-452 Sequence 452, App
39	76	3.2	1070	7	US-11/062 Sequence 4, Appli
40	76	3.2	1095	7	US-11/062 Sequence 7, Appli
41	76	3.2	1169	7	US-11-077-550-20 Sequence 20, Appli
42	76	3.2	1586	6	US-10-821-234-901 Sequence 901, App
43	75.5	3.2	306	7	US-11-014-402-4 Sequence 4, Appli
44	75.5	3.2	449	6	US-10-873-528-110 Sequence 110, App
45	75.5	3.2	518	7	US-11-055-822-420 Sequence 420, App

ALIGNMENTS

RESULT 1
US-10-495-597-5

Sequence 5, Application US/10495597
Publication No. US2005025544A1

GENERAL INFORMATION:
APPLICANT: Svendsen, Allan

APPLICANT: Vind, Jesper
APPLICANT: Heldt-Hansen, Hans Peter

APPLICANT: Erlandsen, Lise

TITLE OR INVENTION: Lipolytic Enzyme Variants and Method for their Production

FILE REFERENCE: 10248-204-US

CURRENT APPLICATION NUMBER: US/10/495,597

CURRENT FILING DATE: 2004-05-14

PRIOR APPLICATION NUMBER: PCT/DK03/00028

PRIOR FILING DATE: 2003-01-16

PRIOR APPLICATION NUMBER: US 60/353,557

PRIOR FILING DATE: 2002-02-04

PRIOR APPLICATION NUMBER: DK 2002 00074

PRIOR FILING DATE: 2002-01-16

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.2

SEQ ID NO 5

LENGTH: 267

TYPE: PRT

ORGANISM: Aspergillus niger

US-10-495-597-5

Query Match

Best Local Similarity 26.7%; Pred. No. 0.00017;

Matches 59; Conservative 32; Mismatches 59; Indels 71; Gaps 12;

178 EKVENKKSIHSSWDCRNIN---LGSASKD-----KKGSDDDDDDDPKMGMQMT 229

46 EKYNST-----DINGMILRDSSEKIIITVFGTSDTTLQD-----T 85

230 IYSEDPKSPFTKL-----SARTQLOTKLQKMTKXKDTLSITPAGH 272

86 NYT---LTFPDITLPQNGCEVHGYYIGWVSQDVESLVKQVSGYPTALVT---GH 139

273 SLGATLSVSAFDIVENITTEIPYAVVFCPCVKNKKFOQLPDSYFN-----LN 322

140 SLGASLALTAQL---SATYDNIRLYTFGEPRGN---QAFASYNDLAFQASSPTTQ 192

323 VLVHNVYIDILPYLVKMGVNIIGIEL-ETD---SRKSTFL 360

193 YFRVTHANDGIPNLFPVEQGYAHGCVSWSDPYASNTTV 233

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Query Match          4.9%; Score 116; DB 6; Length 278;
Beet Local Similarity 21.5%; Pred. No. 0.0024;
Matches 60; Conservative 42; Mismatches 117; Indels 60; Gaps 11;

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Db 13 WVOYAAATYCCNNVVAADGELKNSVGNCPD---VEAGSTVLSRSDDTIDTAGFVAP 69
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 181 ENEEKSIHKSSWYDCNINILGSAKDKKSGSDDDDDDPKMGGMW--IYSEDP-- 236
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Db 70 DNTKKAIV-----VAFRGSYS-----IRMWVIDATFPQTPGL 102
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 237 -----KSPFTKLSA-----RTQLQFTLKQMTMKYDETLSTFAGHSIGATLSVSAFDIYE 288
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Db 103 CDGCKAELGFWTAKKVVDRITKTLDELKPEHSD--KYIIVGHSIGALIASIAADL-- 158
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 289 NLATTEIPYAVAFCCPKVGNKKFQQLDPSYPNINVLHVRNVIDLIPLYPKLMGYVNICI 348
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 159 -RTKNVDAILVAAPAPVANKPLAEFTINGGN-NYRPTHN-DDPVPKPLPLTMGYHISP 215
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 349 ELEIDSRKSTFLDKSKNPSDMWHNLQAILHVVGSHGKYGK 387
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 216 EYVITAPDNTTVTVDNQ-----VTVLGDEVNKEG 243
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
US-10-495-597-11
; Sequence 11, Application US/10495597
; Publication No. US20050255544A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Wind, Jesper
; APPLICANT: Heide-Hansen, Hans Peter
; APPLICANT: Erlandsen, Lise
; TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
; FILE REFERENCE: 10248-204-US
; CURRENT APPLICATION NUMBER: US/10/495,597
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/DK03/00028
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/353,557
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: DK 2002 00074
; PRIOR FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2

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RESULT 4
US-10-495-597-14
; Sequence 14, Application US/10495597
; Publication No. US2005025544A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Vind, Jesper
; APPLICANT: Heldt-Hansen, Hans Peter
; APPLICANT: Eriksen, Luise
; TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
; FILE REFERENCE: 10248.204-US
; CURRENT APPLICATION NUMBER: US/10/495,597
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/DK03/00028
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/353,557
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: DK 2002 00074
; PRIOR FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Thermomyces lanuginosus
US-10-495-597-14

```

```

Query March 4.64; Score 110.5; DB 6; Length 269;
Best Local Similarity 25.24; Pred. No. 0.0072;
Matches 28; Conservative 22; Mismatches 56; Indels 5; Gaps 2;

Qy      244  SARTLOTKIKOMTKYKDETLSTFAGSLGATSVSAPFIVENTLTIETVAVFGC 303
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      119  SVADTLRQKEDAVREHPD--YRVVFTGSLGALATVAGALDRG--GYDIDPFSYGA 173

Qy      304  PKYGNKKFQOLPDSYPMLNTLVAVRNIDILPLYVKLMGYNIGIEIDS 354
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      174  PRVGNRAFAEFLTYQTGCTLYRITHNDIDVPLRPREFGSHSSPEYWIKS 224

RESULT 5
US-10-495-597-12
; Sequence 12, Application US/10495597
; Publication No. US20050255544A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Wind, Jesper
; APPLICANT: Heldt-Hansen, Hans Peter
; APPLICANT: Erlandsen, Buiue
; TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production

```

FILE REFERENCE: 10248.204-US
CURRENT APPLICATION NUMBER: US/10/495,597
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: PCT/DK03/00028
PRIOR FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US 60/353,557
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: DK 2002 00074
PRIOR FILING DATE: 2002-01-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENGTH: 270
TYPE: PRT
ORGANISM: Aspergillus niger
US-10-495-597-12

Query Match 4.5%; Score 108; DB 6; Length 270;
Best Local Similarity 30.9%; Pred. No. 0.012;
Matches 29; Conservative 16; Mismatches 41; Indels 8; Gaps 4;

Qy 244 SARQLOTKLKQMTKYDELTSTFAGHSGLATLSVSAFDIENLTETPTAVVFGC 303
Db 119 AADNLTSKIKSAMSTYSGYL--YFTGHSIGALATLGA-TVLRN--DGYSVELYTYGC 173
Qy 304 PKVGNKKFQOLFDSY---PNNLVHVRNVIDLIP 334
Db 174 PRVGNVALAEHITSGSGANFPVTHNDIVPRVP 207

RESULT 6
US-10-495-597-4
Sequence 4, Application US/10495597
Publication No. US20050255544A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Vind, Jesper
APPLICANT: Heidt-Hansen, Hans Peter
APPLICANT: Erlandsen, Luise
TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
FILE REFERENCE: 10248.204-US
CURRENT APPLICATION NUMBER: US/10/495,597
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: PCT/DK03/00028
PRIOR FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US 60/353,557
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: DK 2002 00074
PRIOR FILING DATE: 2002-01-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 270
TYPE: PRT
ORGANISM: Rhizopus oryzae
US-10-495-597-4

Query Match 4.3%; Score 101.5; DB 6; Length 270;
Best Local Similarity 28.6%; Pred. No. 0.047;
Matches 28; Conservative 18; Mismatches 45; Indels 7; Gaps 3;
Qy 264 TLSTFGHSIGATLSVSAFDIENLTETPTAVVFGC--CCPVGNKKFQOLFDS--YR 319
Db 137 TYKIVTGHSLGAGQALLAGNDLYOREBRSLPKSLSTFTVGGPVGNGFTFAVYVESTGIP 196
Qy 320 NNLVHVRNVIDLIPYFKLMGYVNICIELEIDSRSK 357
Db 197 FQRTVHKR---DIVPHVDPQSGFGLHPEVESWIKSGIS 231

RESULT 7
US-10-495-597-13
Sequence 13, Application US/10495597

Publication No. US20050255544A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Vind, Jesper
APPLICANT: Heidt-Hansen, Hans Peter
APPLICANT: Erlandsen, Luise
TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
FILE REFERENCE: 10248.204-US
CURRENT APPLICATION NUMBER: US/10/495,597
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: PCT/DK03/00028
PRIOR FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US 60/353,557
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: DK 2002 00074
PRIOR FILING DATE: 2002-01-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
LENGTH: 269
TYPE: PRT
ORGANISM: Aspergillus oryzae
US-10-495-597-13

Query Match 4.1%; Score 98; DB 6; Length 269;
Best Local Similarity 19.9%; Pred. No. 0.096;
Matches 52; Conservative 39; Mismatches 92; Indels 78; Gaps 9;

Qy 100 SVPEAFILKRSRREKWD--RBS---NWIGYVVSNDTSRVAGREVVYVMRTCDYE 153
Db 36 SVGNCPLEVAASSTQSLDEFNSESSEYGNPAGYLA--DETNYL-----LVISFRGSADLAN 88
Qy 154 WVDVIGAGQLESANHLATQOTTHHEKXENNEKSIHSSWYDCFNINILGSASDKKXGS 213
Db 89 WVANLNFGLDASDLCCGCE-----VHSGFW----- 114
Qy 214 DDDDDDDPKWQGMWITYTSEDPSPTKLARSOTQTKLQMTKYDELTSTFAGHS 273
Db 115 -----KAMSELAET-----ISKYSALSDHSDVSLVLT--GHS 146
Qy 274 LGATLSVSAFDIENLTETPTAVVFGCPRVGNKKFQOLFDSYNNLVHVRNVIDLIP 333
Db 147 YGALLALALATATL---RNSGVSVELVNYGQPRIGNEALATYITDQNGKGNVRVTHNDIV 203
Qy 334 PLVPVKLMGYVNICIELEIDS 354
Db 204 PKLPPTLGYHHSPEYTISS 224

RESULT 8
US-10-495-597-1
Sequence 1, Application US/10495597
Publication No. US20050255544A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Vind, Jesper
APPLICANT: Heidt-Hansen, Hans Peter
APPLICANT: Erlandsen, Luise
TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
FILE REFERENCE: 10248.204-US
CURRENT APPLICATION NUMBER: US/10/495,597
CURRENT FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: PCT/DK03/00028
PRIOR FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US 60/353,557
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: DK 2002 00074
PRIOR FILING DATE: 2002-01-16
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 265
TYPE: PRT

ORGANISM: Absidia reflexa
US-10-495-597-1

Query Match 4.1%; Score 97.5; DB 6; Length 265;

Best Local Similarity 24.3%; Pred. No. 0.1;
Matches 35; Conservative 26; Mismatches 56; Indels 27; Gaps 6;

QY 222 KVMGMMTIYTSSEDPKSPFTLSARTQTKLKQMLTKYKQDETSLTFPAGSLGATLSV 281
DB 108 KVMGFMDSIVNEVDK-----LVAEVKQDLRHPGKIVT--GHSLSGATAVL 154
QY 282 SAPDIVENTLTTEIPYAVVFCSPKVGKKFOO--LFDSYPMNLAVHVNIDLPLYPVK 339
DB 155 SALLYNNHGANIEI--YTGQPRIGTAPFANVYIGTKIPYORLVHER--DIVPHLPRG 209
QY 340 LMGVNTIGIELEIDSRKSTFLKDS 363
DB 210 AFGFLHAGEEPMI-----MKDS 226

RESULT 9

US-10-495-597-6
; Sequence 6, Application US/10495597
; Publication No. US20050255544A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Vind, Jesper
; APPLICANT: Heide-Hansen, Hans Peter
; TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
; FILE REFERENCE: 10248.204-US
; CURRENT APPLICATION NUMBER: US/10/495,597
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/DK03/00028
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/353,557
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: DK 2002 00074
; PRIOR FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Aspergillus tubingensis
US-10-495-597-6

Query Match 4.1%; Score 97; DB 6; Length 312;

Best Local Similarity 21.1%; Pred. No. 0.15;
Matches 53; Conservative 40; Mismatches 70; Indels 88; Gaps 12;

QY 123 GYVVNSDETSEVAVGREYVYVWRGTCRDYEWVDVLGAQLSEAHPLLTQOOTHYKVEN 182
DB 103 GY--VATDSS-----KEIITVFRGTGSD-----TNQLDTNYTL-----TPDITLPQ 143
QY 183 EEKKSIIHSSWYDCENILNLSASKDKGSGDDDDDDPKVQGMITIYTSSEDPKSPFTK 242
DB 144 CNSCEVHGGYI-----GN----- 157
QY 243 LSARTQTKLKQMLTKYKQDETSLTFPAGSLGATLSVVSAPDIVENTLTTEIPYAVVFG 302
DB 158 ISVQGVSVLQGVQSGPFDVLTVT--GHSLSGASLALTAAGL--SATYONILLYTFEG 212
QY 303 CPKVGKKFQQLFDSYPN-----LNLVHVNVDLPLYPVKLMGVNTIGIELE-E 351
DB 213 EP-----KSNQAFASYMDAFQASSPDTTYQYFRVTHANDGIPNLPRADEGVAHGVVEYS 267
QY 352 ID--SRKSTFL 360
DB 268 VDPYSAQNTFV 278

RESULT 10

US-10-770-726-77
; Sequence 77, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10/770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 4128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-770-726-77

Query Match 3.9%; Score 94; DB 6; Length 4128;

Best Local Similarity 21.1%; Pred. No. 9.6;
Matches 96; Conservative 54; Mismatches 150; Indels 156; Gaps 23;

QY 80 FPGGADRFVAVYLYATAK---VSVEAFLLSRSEKMDRESNMIGYVVNSDETSEV 135
DB 1729 FPGTFRFN--NYVDCMKKFLDALIELSQSPMLLEMTVELCREQOHV-----MEELFQS 1780
QY 136 AGREVVYVWRGTCRDYEWVDVLGAQLSEAHPLLTQOOTHYKVENVEEKKSIHKSQWYD 195
DB 1781 SFRR--IARRGSC---VTQVGL-LESVYEMR-----KDDPRLSFTKQSFVD 1821
QY 196 CFNINILGSASKDKGSGDDDDDDPKVQGMITIYTS--EDPKSPFTKLSARTQTKL 253
DB 1822 RSLITLHRCSLD-----ALREFFSITVDAIDVLKSRFTKLNESF--PDTQI 1867
QY 254 KQMLTKYKQDETSLTFP-----GHSLSGATLSVVSAPDIV 288
DB 1668 TKKGYYK--ILDVWYSLRPDGVHAKESKINQVHSGSCITEGNETLTKLICYDAFTB 1925
QY 289 NLTFE-----IPYAVVFCSPKVGKKFOO--LFDSYPMNLAVHVN 328
DB 1926 NMAGENQLERRRLYHCAVNCALSVICVF---NELKYGQFLSEKPEKNLLIFEN 1980
QY 329 VIDLIPYVYKLMGVNTIGIELEID--SRKSTFLK-----DSKNPSDMHNL----- 372
DB 1981 LIDLKRY-----NFPVEVEVPMERKKYIIRKEAREANAGSDGSPYMSLSYLA 2032
QY 373 -----QAILHVVSGMHGKGEFKVVKRSVA---LVNKSDFL-KEE 410
DB 2033 DSTLSEMSQPDFSTGVQSVYSQDPRPAPGRFRRRRQDPVTVHDDVLELMDLNRHE 2092
QY 411 CLVPRAMVYVQNKGMVNLKQGEWTLAP--BEDTTP 444
DB 2093 CMAPLT-----ALVKHMRSLGPPQGEEDSV 2119

RESULT 11

US-10-495-597-2
; Sequence 2, Application US/10495597
; Publication No. US20050255544A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Vind, Jesper
; APPLICANT: Heide-Hansen, Hans Peter
; TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
; FILE REFERENCE: 10248.204-US
; CURRENT APPLICATION NUMBER: US/10/495,597
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/DK03/00028
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/353,557

Query Match	3.8%	Score 89.5	DB 6	Length 269
Best Local Similarity	17.4%	Pred. No. 0.56		
Matches	58	Conservative	48	Mismatches 99; Indels 129; Gaps 13;
Qy	28	GLNPLNDELRELILRCGDFCQVYTDYTFINDONSSTGSGSRGKADLLHKTPAPEGADRF	87	
Db	5	GIRATSTQEOINEL-----TYTTTLL--NSNYC-----RTYIPGAT--W	38	
Qy	88	DVAAYILYATAKVSYPEAFLLKRSREKMDSESNIGVYVNSDETSRVAGREVVYVWVG	147	
Db	39	DCI-HCATDETDLKIK-----TWSTLIYDTNMAVRGSEKTIYIVFRG	81	
Qy	148	TCRRYEVVDVYGAQLSESAHPLRTQOTTHYEKXENEEKSIIHSSMYDDCFNINLLGSASK	207	
Db	82	SSSRIMWIADITFPVPSYFVSGT-----	105	
Qy	208	DKGSGSDDDDDDBEKVMQGMNTIYTSDDPKSPPTKLSARTOLOTKLKKMLTKYKDETLSTI	267	

```

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3303R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIORITY FILING DATE: 2002-04-24
PRIORITY FILING DATE: 1997-06-18
PRIORITY APPLICATION NUMBER: 60/056974
PRIORITY FILING DATE: 1997-08-26
PRIORITY APPLICATION NUMBER: 60/059113
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059115
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059117
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059122
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059184
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059263
PRIORITY FILING DATE: 1997-09-18
PRIORITY APPLICATION NUMBER: 60/059352
PRIORITY FILING DATE: 1997-09-19
PRIORITY APPLICATION NUMBER: 60/059588
PRIORITY FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 138
LENGTH: 478
TYPE: PRT
ORGANISM: Homo Sapien
US-10-131-826A-138

Query Match      3.7%; Score 87.5; DB 6; Length 478;
Best Local Similarity 22.1%; Pred. No. 1.9;
Matches    52; Conservative   43; Mismatches    85; Indels    55; Gaps    13

221 PKMQGMMHTIYISEDPK-----SPTKLSARTQLOTKLKQMLTKYKHDETSLITFAGH 272
DB PK--EEMQVYSNAQDDGCICTTVVAPEQNLCSPANSRSRLRRLLERYQNNSSIEV-- 1022

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Qy 273 SLGATLSVSAFDIVENTTEIPYTAVFVGGCPKYNKKFQQLFDSYPNLNLVLR-----N 328
Db 103 ---LNLRTQRFQVYLNKMETQM-----KGIKAKFRRIEDDRKLTMKRHOELKEX 149
Qy 329 VIDILIPYVKLMGVNIGILEIDSRKSTFLKDSKNPSDMHNLQAILHVVSCHHGKXGE 388
Db 150 MDELPLPLPV-LEQY-----KTDAKLITQFKE-----EIRNLSAVLTLGIOEBIGAY-D 195
Qy 389 FKVVNKRSAVALVNSCDFLKE-EC-----LVPRAMVVQNGKMWLNKDGENVLAP 437
Db 196 YEEHLQVRVLSLETRLRDCMKKLTGCKLMKITGPV--TVKTSG---TRFGAMWMDP 245

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RESULT 14

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US-11-174-150-27
; Sequence 27, Application US/11174150
; Publication No. US2005026071A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Ritvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoxing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: US/11/174,150
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/10/257,174
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/US01/11797
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-174-150-27

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```

Query Match 3.7%; Score 87.5; DB 7; Length 478;
Best Local Similarity 22.1%; Pred. No. 1.9; Indels 55; Gaps 13;
Matches 52; Conservative 43; Mismatches 85;
Qy 221 PKVMQGMNTIYSEDPK-----SPTKLSARTQLTKLQMLTKYKDETLSTTFAGH 272
Db 48 PK--EGWQVYSAQDPDRCTVAPFQNLCSRADKSRQLRLLEKVNMSQSIEV--- 102
Qy 273 SLGATLSVSAFDIVENTTEIPYTAVFVGGCPKYNKKFQQLFDSYPNLNLVLR-----N 328
Db 103 ---LNLRTQRFQVYLNKMETQM-----KGIKAKFRRIEDDRKLTMKRHOELKEX 149
Qy 329 VIDILIPYVKLMGVNIGILEIDSRKSTFLKDSKNPSDMHNLQAILHVVSCHHGKXGE 388
Db 150 MDELPLPLPV-LEQY-----KTDAKLITQFKE-----EIRNLSAVLTLGIOEBIGAY-D 195
Qy 389 FKVVNKRSAVALVNSCDFLKE-EC-----LVPRAMVVQNGKMWLNKDGENVLAP 437
Db 196 YEEHLQVRVLSLETRLRDCMKKLTGCKLMKITGPV--TVKTSG---TRFGAMWMDP 245

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RESULT 15
US-10-495-597-10
; Sequence 10, Application US/10495597
; Publication No. US2005025554A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Vind, Jesper
; APPLICANT: Heldt-Hansen, Hans Peter

```

```

; APPLICANT: Erlandsen, Lise
; TITLE OF INVENTION: Lipolytic Enzyme Variants and Method for their Production
; FILE REFERENCE: 10248.204-US
; CURRENT APPLICATION NUMBER: US/10/495,597
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/DK03/00028
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/353,557
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: DK 2002 00074
; PRIOR FILING DATE: 2002-01-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Penicillium camemberti
US-10-495-597-10

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Query Match 3.6%; Score 87; DB 6; Length 278;
Best Local Similarity 24.4%; Pred. No. 0.99;
Matches 29; Conservative 24; Mismatches 58; Indels 8; Gaps 4;
Qy 246 RTQLQTLKQMLTKYKDETLSTTFAGHSLGATLSVSAFDIVENTTEIPYTAVFVGGCPK 305
Db 120 RDIILKELKEVVA--QPNYVELVVVGHSLGAAVATLATDLRGKGYPSAKLYA--YASPR 175
Qy 306 VGNKKFQQLFDSY-PNLNLVLRNVIDLIPYVKLMGVNIGILEIDSRKSTFLKDS 363
Db 176 VGNALAKYITTAQNNRFRHTN---DPVRKLPLLSMGYHVSPSEVWITSNNATVSTS 231

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Search completed: December 22, 2005, 19:53:13
Job time : 9 secs

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OM protein - protein search, using sw model

Run on: December 22, 2005, 19:37:37 ; Search time 112.5 Seconds
(without alignments)
1660.175 Million cell updates/sec

Title: US-10-674-540A-2
Perfect score: 2385
Sequence: 1 MAEAQPLGSKGPTWPEL.....NKDEWVLAPEEDPTPEFD 447

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.Main:*
1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	2385	100.0	447	US-10-674-540-2	Sequence 2, Appl1
2	2377	99.7	447	US-10-674-540-11	Sequence 11, Appl1
3	1310	54.9	419	US-10-424-599-153165	Sequence 153165,
4	1077	45.2	348	US-10-674-540-16	Sequence 16, Appl1
5	1060	44.4	456	US-10-437-963-162831	Sequence 162831,
6	824.5	34.6	395	US-10-425-115-289922	Sequence 289922,
7	824.5	34.6	410	US-10-425-114-72507	Sequence 72507, A
8	775.5	32.5	422	US-10-437-963-115585	Sequence 115585,
9	775	32.5	418	US-10-674-540-12	Sequence 12, Appl1
10	767.5	32.2	423	US-10-739-930-6050	Sequence 6050, Ap
11	766	32.1	434	US-10-739-930-9783	Sequence 9783, Ap
12	740.5	31.0	407	US-10-437-963-138670	Sequence 138670,
13	736	30.9	420	US-10-437-963-139028	Sequence 139028,
14	727	30.5	418	US-10-437-963-153035	Sequence 153035,
15	721.5	30.3	430	US-10-425-115-205760	Sequence 205760,
16	710.5	29.8	357	US-10-437-963-103394	Sequence 103394,
17	705	29.6	402	US-10-425-115-288260	Sequence 288260,
18	705	29.6	434	US-10-425-114-56307	Sequence 56307, A
19	705	29.6	497	US-10-424-599-155234	Sequence 155234,
20	705	29.6	515	US-10-424-599-145851	Sequence 45851, A
21	703	29.5	576	US-10-425-115-344208	Sequence 344208,
22	686.5	28.8	447	US-10-674-540-19	Sequence 19, Appl1
23	684	28.7	448	US-10-674-540-14	Sequence 14, Appl1
24	681	28.6	603	US-10-437-963-150201	Sequence 150201,
25	659	27.6	463	US-10-425-114-47664	Sequence 47664, A
26	658	27.6	466	US-10-424-599-191071	Sequence 191071,
27	639	26.8	504	US-10-425-115-250498	Sequence 250498,

28	639	26.8	505	4	US-10-425-115-250500	Sequence 250500,
29	626	26.2	395	4	US-10-425-115-364917	Sequence 364917,
30	610.5	25.6	397	4	US-10-425-114-64410	Sequence 64410, A
31	580.5	24.3	195	4	US-10-674-540-17	Sequence 17, Appl1
32	576.5	24.2	401	4	US-10-674-540-13	Sequence 13, Appl1
33	526	22.1	247	4	US-10-767-701-31587	Sequence 31587, A
34	503.5	21.1	221	4	US-10-425-115-240503	Sequence 240503,
35	462	19.4	544	4	US-10-437-963-174406	Sequence 174406,
36	441.5	18.5	534	4	US-10-437-963-173543	Sequence 173543,
37	425.5	17.8	351	4	US-10-424-599-241094	Sequence 241094,
38	411	17.2	187	4	US-10-437-963-115584	Sequence 115584,
39	403	16.9	481	4	US-10-437-963-195459	Sequence 195459,
40	395	16.6	183	4	US-10-437-963-138668	Sequence 138668,
41	389.5	16.3	430	4	US-10-424-599-164443	Sequence 164443,
42	389.5	16.3	443	4	US-10-425-114-54277	Sequence 54277, A
43	388.5	16.3	154	4	US-10-767-701-59572	Sequence 59572, A
44	380.5	16.0	518	4	US-10-424-599-273196	Sequence 273196,
45	378.5	15.9	348	4	US-10-425-114-51257	Sequence 51257, A

ALIGNMENTS

```
RESULT 1
US-10-674-540-2
; Sequence 2, Application US/10674540
; Publication No. US20040158891A1
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE.
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/10/674,540
; CURRENT FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Plant
US-10-674-540-2
Query Match          100.0%; Score 2385; DB 4; Length 447;
Best Local Similarity 100.0%; Pred. No. 3.7e-219;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	MAEAQPLGSKGPTWPELGGNAAGLNPINDELRELLRCGDFCQVYDTFINDN	60
DB	1	MAEAQPLGSKGPTWPELGGNAAGLNPINDELRELLRCGDFCQVYDTFINDN	60
QY	61	SSYGGSSRYKADILHTAIPGAGRDVYALYATKXSVPAFLKSSREKMDEN	120
DB	61	SSYGGSSRYKADILHTAIPGAGRDVYALYATKXSVPAFLKSSREKMDEN	120
QY	121	WIGVVVSNDETNRVAGREVVYVWRGTCRDYEVNDVLAGQLSAPHLTQOTTHEKV	180
DB	121	WIGVVVSNDETNRVAGREVVYVWRGTCRDYEVNDVLAGQLSAPHLTQOTTHEKV	180
QY	181	ENEEKKSIHKSWMYDCFNILGASAKDKGSDDDDDPKVMQGMWITYSEDPKSP	240
DB	181	ENEEKKSIHKSWMYDCFNILGASAKDKGSDDDDDPKVMQGMWITYSEDPKSP	240
QY	241	TKLSARTOLOTKLKQMTKTKKDETLSTTPAGHSIGATLSVSAFDIYENITTEIPYNAV	300
DB	241	TKLSARTOLOTKLKQMTKTKKDETLSTTPAGHSIGATLSVSAFDIYENITTEIPYNAV	300

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Qy 301 FGCPRVGNKKFQQLFDSYPNLNVLHVRNVIDLIPYVKLMGYVNIIELEIDSRKSTFL 360
Db 301 FGCPRVGNKKFQQLFDSYPNLNVLHVRNVIDLIPYVKLMGYVNIIELEIDSRKSTFL 360
Qy 361 KDSKNPSPDMHNLQAILHVVSGMHGKGFVKVYNKRSVALVYKSCDFLKEECLVPPAMVV 420
Db 361 KDSKNPSPDMHNLQAILHVVSGMHGKGFVKVYNKRSVALVYKSCDFLKEECLVPPAMVV 420
Qy 421 QNKGWVLNKDGEMVLAPPEEDPTPEFD 447
Db 421 QNKGWVLNKDGEMVLAPPEEDPTPEFD 447

RESULT 2
US-10-674-540-11
; Sequence 11, Application US/10674540
; Publication No. US20040158891A1
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/10/674,540
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Plant
; US-10-674-540-11

Query Match 99.7%; Score 2377; DB 4; Length 447;
Best Local Similarity 99.8%; Pred. No. 2,1e-218; Indels 0; Gaps 0;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAAEKQPIGLSKPGTPELIGSNMAGLNPINDELRELLRCGDFCQVYTFINDQN 60
Db 1 MAAEKQPIGLSKPGTPELIGSNMAGLNPINDELRELLRCGDFCQVYTFINDQN 60
Qy 61 SSYCGSSRYGKADLHKTAFPGADRPVVAVLYATAKVSPEAFILKRSRREKNDRESN 120
Db 61 SSYCGSSRYGKADLHKTAFPGADRPVVAVLYATAKVSPEAFILKRSRREKNDRESN 120
Qy 121 WIGYVVSNDSTSRVAGREYVYVWRGTCRDYEWVDYVGAQLESAPHLRTQOTTHVSKV 180
Db 121 WIGYVVSNDSTSRVAGREYVYVWRGTCRDYEWVDYVGAQLESAPHLRTQOTTHVSKV 180
Qy 121 WIGYVVSNDSTSRVAGREYVYVWRGTCRDYEWVDYVGAQLESAPHLRTQOTTHVSKV 180
Db 121 WIGYVVSNDSTSRVAGREYVYVWRGTCRDYEWVDYVGAQLESAPHLRTQOTTHVSKV 180
Qy 181 ENEEKSHKSWYDCENINILGASAKDGKSDDDDDDPVMOGMWTIYTSSEDPKSPF 240
Db 181 ENEEKSHKSWYDCENINILGASAKDGKSDDDDDDPVMOGMWTIYTSSEDPKSPF 240
Qy 181 ENEEKSHKSWYDCENINILGASAKDGKSDDDDDDPVMOGMWTIYTSSEDPKSPF 240
Db 181 ENEEKSHKSWYDCENINILGASAKDGKSDDDDDDPVMOGMWTIYTSSEDPKSPF 240
Qy 241 TKLSARTQLQTKLQKLMATKYKDELTSTFAGHSLGATLSVSAFDIVENLTTEIPVTAVV 300
Db 241 TKLSARTQLQTKLQKLMATKYKDELTSTFAGHSLGATLSVSAFDIVENLTTEIPVTAVV 300
Qy 301 FGCPRVGNKKFQQLFDSYPNLNVLHVRNVIDLIPYVKLMGYVNIIELEIDSRKSTFL 360
Db 301 FGCPRVGNKKFQQLFDSYPNLNVLHVRNVIDLIPYVKLMGYVNIIELEIDSRKSTFL 360
Qy 361 KDSKNPSPDMHNLQAILHVVSGMHGKGFVKVYNKRSVALVYKSCDFLKEECLVPPAMVV 420
Db 361 KDSKNPSPDMHNLQAILHVVSGMHGKGFVKVYNKRSVALVYKSCDFLKEECLVPPAMVV 420
Qy 421 QNKGWVLNKDGEMVLAPPEEDPTPEFD 447
Db 421 QNKGWVLNKDGEMVLAPPEEDPTPEFD 447
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Db 421 QNKGWVLNKDGEMVLAPPEEDPTPEFD 447

RESULT 3
US-10-424-599-153165
; Sequence 153165, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Tongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 153165
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_109332C.1.pep
; US-10-424-599-153165

Query Match 54.9%; Score 1310; DB 4; Length 419;
Best Local Similarity 58.1%; Pred. No. 3e-116;
Matches 251; Conservative 54; Mismatches 99; Indels 28; Gaps 3;

Qy 15 PTWPELIGSNMAGLNPINDELRELLRCGDFCQVYTFINDQNSSYCGSSRYGKADL 74
Db 9 PTWPELIGSNMAGLNPINDELRELLRCGDFCQVYTFINDQNSSYCGSSRYGKADL 74
Qy 75 LKHTAFPGADRPVVAVLYATAKVSPEAFILKRSRREKNDRESNITGVVVSNDSTSR 134
Db 69 FRKVM-LDCEPNYDVAFLVATARVTVBEAFLHSLSREAMDRESNIGYIAVTSDSRSQ 127
Qy 135 VAGREYVYVWRGTCRDYEWVDYVGAQLESAPHLRTQOTTHVSKVENEKSHKSWY 194
Db 128 ELGRRELYVWRGTCRDYEWVDYVGAQLESAPHLRTQOTTHVSKVENEKSHKSWY 165
Qy 195 DCFNINILGASAKDGKSDDDDD--DPKVMQGMWTIYTSSEDPKSPFTKLSARTQLQTK 252
Db 166 ---SLKELKXGNKDGSSSSDEEDDPKPKVMGMLTITYSNDPKSPFTKLSARTQLQAH 222
Qy 253 LKQMTKYKDELTSTFAGHSLGATLSVSAFDIVENLTTEIPVTAVVFGCPRVGNKKFQ 312
Db 223 VKSLQHYSSSENPSTLVVGHSLGATLSVSAFDIVENLTTEIPVTAVVFGSPOVGNKAFN 282
Qy 313 QLPDSYVNLNVLHVRNVIDLIPYVKLMGYVNIIELEIDSRKSTFLKDSKNPSPDMHNL 372
Db 283 ERFNMFNLLKLVHAKVNVIDLIPYVKLMGYVNIIELEIDSRKSTFLKDSKNPSPDMHNL 342
Qy 373 QAILHVVSGMHGKGFVKVYNKRSVALVYKSCDFLKEECLVPPAMVVQNKGWVLNKDG 432
Db 343 QAMHVVAGNMNKKKEEFEMVKSVALVYKSCDFLKEEYVPGSVMVYKQKGVKVRBDGE 402
Qy 433 WVLAPPEEDPT 444
Db 403 WVLAPPEEDPT 414

RESULT 4
US-10-674-540-16
; Sequence 16, Application US/10674540
; Publication No. US20040158891A1
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
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[illegible]

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Db      66  FNRDPLSRVDV-SNPNIYEITKFIYAMCTVSLPDGFWKSLSKAAMSQNMNGFVAVA 124
Oy      129  NDETSRVAGREVVYVWVGTCRDYEWVDVLAQLESAPHLRTQOTTHVEKENEKESI 188
Db      125  TDEGKEILGRDVVVAMGTRMVEWDDLSIVPASEIV----- 165
Oy      189  HKSSWYDFCNILGASAKGKSGSDDDDPKVMQGMNTIYSEDPKSPFTKLARTQ 248
Db      166  -----LPSAA-----NPCVHGMLSVYTSADGSGYNKESARHQ 200
Oy      249  LQTKLKQMLTKYKDETLSTIFAGHSLGATLSVSAFDIVENLTTE--IPYTAVPGCKV 306
Db      201  VLNEVKRIQDLYKPEETSIITIGHSLGALATINATDIVSNGYNKSCCPVSAFVGSBRV 260
Oy      307  GNKKFQOLFDSYPNLVNVAHVNVIDLIPYPVKLMGVNIGIELEIDSRKSTFLKDSKRP 366
Db      261  GNLDFOKAFDSADRLRLRNRNSPDVVKWP--KLGYSDVGTLMIDTGSFPYLKAPGNP 318
Oy      319  LTHWDMCYMHGVAGAGSSGGFELLVD RDVALVNHEDALRNEFAVPFPMWVYQNKGMV 378
Oy      427  LNKGEVTLAPPEED 441
Db      379  KGKDGWRMLADHEED 393

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RESULT 7

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US-10-425-114-72507
; Sequence 72507, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72507
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73170B05_FIL.pep
US-10-425-114-72507

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Query Match      34.6%; Score 824.5; DB 4; Length 410;
Best Local Similarity 39.5%; Pred. No. 9e-70;
Matches 172; Conservative 70; Mismatches 144; Indels 49; Gaps 5;

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Oy      9  GLSKGPTMPPELLGSNANAGLNPINDELRELLRCGDFCQYTYTFTINDQSSYCGSSR 68
Db      21  GGNVAKKMKELNGLNWKGVLDPDLDIRRNIINYGELSQATYGLNRRERSRYAGSGL 80
Oy      69  YGKADLLHKTAPPGADRFDVAVLYATAKV-SVPEAFLLKSRSREKMDRESNMIGYVVS 128
Db      81  FRRRPFRLSRVDV-SNPNIYEITKFIYAMCTVSLPDGFWKSLSKAAMSQNMNGFVAVA 139
Oy      129  NDETSRVAGREVVYVWVGTCRDYEWVDVLAQLESAPHLRTQOTTHVEKENEKESI 188
Db      140  TDEGKEILGRDVVVAMGTRMVEWDDLSIVPASEIV----- 180
Oy      189  HKSSWYDFCNILGASAKGKSGSDDDDPKVMQGMNTIYSEDPKSPFTKLARTQ 248
Db      181  -----LPSAA-----NPCVHGMLSVYTSADGSGYNKESARHQ 215
Oy      249  LQTKLKQMLTKYKDETLSTIFAGHSLGATLSVSAFDIVENLTTE--IPYTAVPGCKV 306

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Db      216  VLNEVKRIQDLYKPEETSIITIGHSLGALATINATDIVSNGYNKSCCPVSAFVGSBRV 275
Oy      307  GNKKFQOLFDSYPNLVNVAHVNVIDLIPYPVKLMGVNIGIELEIDSRKSTFLKDSKRP 366
Db      276  GNLDFOKAFDSADRLRLRNRNSPDVVKWP--KLGYSDVGTLMIDTGSFPYLKAPGNP 333
Oy      367  SDWNLQAILHVVSGMHGVKGEFVKVNRKSVVALYNKSCDFLKEECLVPAMWYQNKGMV 426
Db      334  LTHWDMCYMHGVAGAGSSGGFELLVD RDVALVNHEDALRNEFAVPFPMWVYQNKGMV 393
Oy      427  LNKGEVTLAPPEED 441
Db      394  KGKDGWRMLADHEED 408

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RESULT 8

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US-10-437-963-115585
; Sequence 115585, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 115585
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_19168C.1.pep
US-10-437-963-115585

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Query Match      32.5%; Score 775.5; DB 4; Length 422;
Best Local Similarity 37.4%; Pred. No. 4.6e-65;
Matches 172; Conservative 70; Mismatches 135; Indels 83; Gaps 8;

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Oy      17  WPELLGSNANAGLNPINDELRELLRCGDFCQYTYTFTINDQSSYCGSSRYGKADLLH 76
Db      13  WREIHGEDHMKGLDPLDADLRSGVIGYGLAQATNDAFIREAWSPPAGACRYSRDRFLE 72
Oy      77  KT-APPGADRFDVAVLYATAKV-SVPEAFLLKSRSREKMDRESNMIGYVVSNDSTSR 134
Db      73  KAQASTQLAGLYEYTAFAFYATAGAGVAPAPMVR-----NRSNMNGYAVAVATDAGVA 125
Oy      135  VAGREVVYVWVGTCRDYEWVDVLAQLESAPHLRTQOTTHVEKENEKESIHKSSWY 194
Db      126  ALGRDVVVAMGTRMVEWDDLSIVPASEIV----- 156
Oy      195  DCFNINILGASAKGKSGSDDDDPKVMQGMNTIYSEDPKSPFTKLARTQ----- 248
Db      157  ----AGVLGAGGRSPA-----PRVHRGWLSTIYASDPASKYSTLSAREQSHIVDW 202
Oy      249  -----LQTKLKQMLTKYKDETLSTIFAGHSLGATLSVSAFDIVE 288
Db      203  DATSTKPSIYITIGLDYTVYISDEIKRLMDIKYKDEETSIIVGSHLGAATAVATINADIVS 262
Oy      289  NLTE--IPYTAVPGCKVGNKKFQOLFDSYPNLVNVAHVNVIDLIPYPVKLMGVN 345
Db      263  NGLNQHGACPYTAFAFCFRVGDGGRFLPDELGLRLRLRCNSPDVVKPP--MGYAD 320
Oy      346  IGIELEIDSRKSTFLKDSKRPSDWNLQAILHVVSGMHGVKGEFVKVNRKSVVALYNKSCD 405

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Db 321 VGVLEPVDTRRSPLYKSPGNQAVHSHLECYMHGVAAGAKGCKGFKLEVDRLVALVNRKVD 380
Qy 406 FKEECVLPRAWVYVQNKGNVLNDGEMVLAPEEDPTPE 445
Db 381 ALKEEVHPSPWSVQRDKGVAGDGHKMLDYGESSQ 420

RESULT 9
US-10-674-540-12

Sequence 12, Application US/10674540
Publication No. US20040158891A1
GENERAL INFORMATION:
APPLICANT: John E. THOMPSON et al.
TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 10799-10
CURRENT APPLICATION NUMBER: US/10/674,540
CURRENT FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: 09/597,774
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 09/250,280
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 09/105,815
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PaeceSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 418
TYPE: PRF
ORGANISM: Plant
US-10-674-540-12

Query Match 32.5%; Score 775; DB 4; Length 418;
Best Local Similarity 37.5%; Pred. No. 5.1e-65;
Matches 167; Conservative 76; Mismatches 138; Indels 64; Gaps 9;

Qy 17 WPELLGSNANAGLNPINDELRELLRCGDFCQYTYTFINDONSSYCGSSRYKADLLH 76
Db 23 WRDLSSGNHMKMQLPDDIREYIHYGEMAGQYDFPFININTESQFAGASYSRKDPFA 82
Qy 77 KT----APGGADEFVAVLYATAKVSVEPAFLKSRREKMDRESNMIGYVVSNDERT 132
Db 83 KVGLEIHP--YTKYKTKFIATSDIHVPESFLFPISRGSKESNMKGVAVTDDQG 140
Qy 133 SRVAGREVVYVWGTCDYEWVDVLAQLESAPHLRTQOTTVEKVENEEKSIHKSS 192
Db 141 TALGRDDIVVWSRGSVQPLEWVEDPFRGLVNA----- 173
Qy 193 WYDGFNINLGSASKDKGSDDDDDPRKMGOMMTITYSEDPKSPPTKLSARTQLOTK 252
Db 174 -----IKIFG-----BRNDQVQIHQWYSIYMSQDRSPPTKNADQVLR 215
Qy 253 LKQIMTKYKDETLSTIFAGHSLGATLSVSAFDIVEN-----LTTEIPTAVVFGCP 304
Db 216 VGRLETKYKDEVTITCGHSLGALATDSALDIVANGYRPKSRPDKSCVTAFVPSRP 275
Qy 305 KVGKFKFQQLFDSYRNVLVHVRNVIDLIPYVYKMGYVNIIGLEIDSRKSTFLDKSK 364
Db 276 RVGSDPRKLFSGLEDIRVLRTRMLFDVPIYPP--IGSYEVGDEFPIDTRKSPYMKSPG 333
Qy 365 NPSMHNLOALIHVVSCHGV--KGE--PRVYVNRKSVVALVNSCDPLKEKCLVPPAMVYVQN 422
Db 334 NLATFHCEGLYHVAAGTQGNKADLFFLDVERAIGLVNKSVDGLKDCWVPGKRVYLN 393
Qy 423 KGMVNLKDGEMVLAPEEDPTPEPD 447
Db 394 KG-AQDDGSWEVLVDHEDNEDLD 417

RESULT 10
US-10-739-930-6050
Sequence 6050, Application US/10739930

Publication No. US20040216190A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 6050
LENGTH: 423
TYPE: PRF
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: Clone ID: ARATH-23APR03-C213147_1.p
US-10-739-930-6050

Query Match 32.2%; Score 767.5; DB 5; Length 423;
Best Local Similarity 36.7%; Pred. No. 2.7e-64;
Matches 162; Conservative 73; Mismatches 151; Indels 55; Gaps 6;

Qy 17 WPELLGSNANAGLNPINDELRELLRCGDFCQYTYTFINDONSSYCGSSRYKADLLH 76
Db 9 WKVLSGNKMKKGLDPLDRLRYIHYGEMSQGYDAFWWDRKRYAGCYSKRLFA 68
Qy 77 KTAEPGGADEFVAVLYATAKVSVEPAFLKSRREKMDRESNMIGYVVSNDERTSRV 135
Db 69 RTGFLKANPRRYKTYIATASIKLPISTVLSLSDASHVQNMNGYLAATDQKAM 128
Qy 136 AGRREVVYVWGTCDYEWVDVLAQLESAPHLRTQOTTVEKVENEEKSIHKSSMYD 195
Db 129 LGRDDIVVNRGTLQPEYEMANDPFPLEPA-----IS 160
Qy 129 LGRDDIVVNRGTLQPEYEMANDPFPLEPA-----IS 160
Qy 196 CFNINLGSASKDKGSDDDDDPRKMGOMMTITYSEDPKSPPTKLSARTQLOTKQ 255
Db 161 VFPVT-----DPKDNPRIGSGWLDIYASRSRSDYDTSAQEOVQGLKR 205
Qy 256 LMTFKYKDETLSTIFAGHSLGATLSVSAFDIV-----ENLT-----TEIPTAVVFGCPKV 306
Db 206 LLELYKDEEISITFTGSLGAVMSVLSAADLVYKKNININLOKKOVPITVFAFGSPRI 265
Qy 307 GNKKFQQLFDSYRNVLVHVRNVIDLIPYVYKMGYVNIIGLEIDSRKSTFLDKSKNP 366
Db 266 GDNHFKVNDVSLQPLNLRIVNPDAVPHPLL--YSEIGEVLEINTLSTYKSLNF 323
Qy 367 SDMHNLOALIHVVSCHGVKGEFKVYVNRKSVVALVNSCDPLKEKCLVPPAMVYVQNKGV 426
Db 324 RNYHNLIELYHGMAGMODTGVFLEIGRDISLVNKGIDALKEVLPSTWRCIANKGML 383
Qy 427 LNDGEMVLAPEEDPTPEPD 447
Db 384 QMDGTWKLVDVHRDDDDVD 404

RESULT 11

US-10-739-930-9783
Sequence 9783, Application US/10739930
Publication No. US20040216190A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 9783
LENGTH: 434
TYPE: PRF
ORGANISM: Triticum aestivum
FEATURE:
OTHER INFORMATION: Clone ID: TRIAE-23APR03-C176_284.p
US-10-739-930-9783

Query Match 32.1%, Score 766; DB 5; Length 434;
 Best Local Similarity 36.3%; Pred. No. 3,9e-64;
 Matches 160; Conservative 76; Mismatches 145; Indels 60; Gaps 5;

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Qy 11 SKRPT-----WPELGSNAGLPLNDELRELLRCGDPQVYDTFTINDQSSY 63
Db 32 SAPAPVGTVASRRREHLGENSMKGLDPLDPLRLASIIISYGENVQAYDAFNTERRSPH 91
Qy 64 CGSSRYGKADLHHTAFPGADRFDVAVYLYATAKVSVEAFLLKSNR--EKMDRESNW 121
Db 92 CGAGFYGEDLLAGVGPVPHGNNEVTKFIYATSSLPSPSFLPLPLPSLPVMSRESNW 151
Qy 122 IGYVVSNDTSRVAQREVYVYVVGTCRDYEMVDVLAQLESAPHLRTQOTTHVEKVE 181
Db 152 MGYVAVATDEGAALALGRDIYVAMRGYQNMENWVNDLDFAPVAPVLSAASQHLAV- 210
Qy 182 NEEKSIHKSSWYDCFNINLLGSASKDGKSDDDDDDPYVMQGMWTITYSEDPKSPFT 241
Db 211 -----VHHGFLSMYTSNKSSEFT 229
Qy 242 KLSARLOQLTKOLMTYKDETLSTPAGSLGATLSVSAPIV-----ENLTTEI 294
Db 230 KTSARDQVKEVRRLVELYKDEVSITTCGSLGAVTLNAVLDVSSGINKPGSTKSF 289
Qy 295 PVTAVFEGCPKVGKKFOQLFDSYPNLVLVHVRNVDLIPYVYKLMGYVNIIGIELEIDS 354
Db 290 PVTAVFASPHVGCRRFSAFNSFPDDLKALHVNAGDVVPMPP--LGYVDVAVELTIRT 347
Qy 355 RKSTFLKDSKNPSMHNLOAILHVVSGMHGVKGEFRVVKNSVALVNSCDFLKEBCLVP 414
Db 348 IRSBYMRKPATVGTTLHNECYLHGVAGSGAGFKLEVDRIALVNNKADALTDHEHPV 407
Qy 415 PAMVWVQKMGVNLKMDGEVYL 435
Db 408 ACWVWPRHKFMVKGEDGRWTL 428

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RESULT 12
 US-10-437-963-138670
 ; Sequence 138670, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 138670
 ; LENGTH: 407
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_40036C.1.pcp
 US-10-437-963-138670

Query Match 31.0%; Score 740.5; DB 4; Length 407;
 Best Local Similarity 37.5%; Pred. No. 9.9e-62;
 Matches 163; Conservative 70; Mismatches 139; Indels 63; Gaps 7;
 Qy 17 WPELGSNAGLPLNDELRELLRCGDPQVYDTFTINDQSSYCGSSRYGKADLH 76
 Db 14 WRELHGDSWGLDPLDPLDRLSSILSYGELVQATYDSFNRERRSPHAGACVYGHGDL- 72

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Qy 77 KTAPEGADRFDVAVYLYATAKVSVEAFI---LKSREKMDRESNWIGYVVSNDTS 133
Db 73 AAGASAAAGSYATYKFFVATSGLPVEAFLLPLPLPSPAWSRESNMGYVAVATDEGV 132
Qy 134 RVAGREVVYVVGTCRDYEMVDVLAQLESAPHLRTQOTTHVEKVENEEKSIHKSSW 193
Db 133 AALGRDIYVAMRGYVESLEWVNDPFTVPVAP- 166
Qy 194 YDCFNINLLGSASKDGKSDDDDDDPK--VMOGMWTITYSEDPKSPFTKLSARLOQT 251
Db 167 -----VLGAAA-----ANPRALVHRGFLSVYTSNKSOKYKASARDQVLE 208
Qy 252 KLOLMTYKDETLSTPAGSLGATLSVSAPIYEN-----LTTEIPYTAIV 300
Db 209 EVRLMELYKDEVTSLVVGSHLSGLASLATINAVDIYANGANCPASSSSQPCPVTAIV 268
Qy 301 FCGPKVGKKKFOQLFDSYPNLVLVHVRNVDLIPYVYKLMGYVNIIGIELEIDSRKSTFL 360
Db 269 FASPRVGDGFFKAFASFPDLRALHVNAGDVVPMPP--LGYVDVAVKLRISTRSPTL 326
Qy 361 KDSKNPSMHNLOAILHVVSGMHGVKGEFRVVKNSVALVNSCDFLKEBCLVPAMVYV 420
Db 327 RSPCTIETLHNECYLHGVAGSGAGFKLEVDRIALVNNKADALDKQKVPVPPRWVS 386
Qy 421 QNKGMVNLKMDGEVYL 435
Db 387 KNRCMVXADADGHMAL 401

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RESULT 13
 US-10-437-963-139028
 ; Sequence 139028, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 139028
 ; LENGTH: 420
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_40360C.1.pcp
 US-10-437-963-139028

Query Match 30.9%; Score 736; DB 4; Length 420;
 Best Local Similarity 37.5%; Pred. No. 2.8e-61;
 Matches 162; Conservative 69; Mismatches 141; Indels 60; Gaps 9;
 Qy 22 GSNAGLPLNDELRELLRCGDPQVYDTFTINDQSSYCGSSRYGKADLHKTAFP 81
 Db 31 GKDRWDGLDPLDPLDRLDIRYELAQATSDALIGDPASFPAGASRYADPAFLRKVR-A 89
 Qy 82 GGAAPDVAVYLYATAKVSVEAFLLK--SRSREKMDRESNWIGYVVSNDTSRVVGR 139
 Db 90 SDPAPVRYVRVATSSVRLPDATFMRPAPSAGAAWGSNMGYVAVADGVAAKGR 149
 Qy 140 EYVYVVGTCRDYEMVDVLAQLESAPHLRTQOTTHVEKVENEEKSIHKSSWYDCFNI 199
 Db 150 DIVVAMGTGRAVEMANDLDTLVPAAGV----- 179
 Qy 200 NLIGASAKDGKSDDDDDDPKVMQGMWTITYSEDPKSPFTKLSARLOQLTKOLMTK 259

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Db 180 -----GCGPGM-----TQPSVHRGFLSVYTSKSSSPFNKLSAEQVLAETRLRLRA 226
Qy 260 YKDELTSTFAGHSGLATLSVSAFDIYEN-----LTTEIPTYAVVFGCPKGVNKKFQ 312
Db 227 YKNCNCSITTTGHSIGALSTLNAIDIVANGYVRGSSRRVPTALALASPRVGDQFK 286
Qy 313 QLPDSYRNVLAVHVRNVIDLR-LYPVKLMGVNIGLEIDSRKSTFLDSKRPDMHN 371
Db 287 RAFDSTSNLSLRNAPDVIPTILPSAF--FKOVGELLVDITRRSPYLKRPAGPQOMHN 344
Qy 372 LQALIHVSGWHGVKGE---FKVYNKRSVALVYNKSCDFLKEECVPPAMVVONKGMVNL 428
Db 345 LECTLHAVAGTQGA-GCGAGGSLVVDRLDALVYNKENVADLRBYQVPAAMVVKKKGMVQN 403
Qy 429 KQGEVVLAPPEE 440
Db 404 ASGRWVLQDHHE 415
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RESULT 14
US-10-437-963-153035
; Sequence 153035, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbaruk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 153035
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_53027C.1.pcp
US-10-437-963-153035

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Query Match 30.5%; Score 727; DB 4; Length 418;  
Best Local Similarity 38.2%; Pred. No. 2e-60;  
Matches 175; Conservative 51; Mismatches 158; Indels 74; Gaps 6;  
Qy 17 WPELLGSNAGLNPINDELRELLRCGDFCQVYDTFINDONSSYCGSSRYGKADLLH 76  
Db 5 WREIHGSGHMDGLDPLDVRCLITYGEMIMATYEAFFGEHRSPPNAGMCRVHADLFR 64  
Qy 77 K--TAFPGGADRFVVAIYATKAVSYPEAFLKSRSEKDRSNMIGYVVSNDETSR 134  
Db 65 RVDVSHPGW--YATRIYATANADVHGKVLRLPCREGATECMNMGYVAVAITDGA 121  
Qy 135 VAGREYVYVWRGCRDYEVDVGAQLESAPHLRTQOTTHVEKVENEBKKSJHKSWMY 194  
Db 122 ALGRRDVIVANRGORALEWADLKAPASAGIL----- 156  
Qy 195 DCFNINILGSASKDKGSDDDDDPKVMQGMNTYTSSEDPKSPFTKLSARTG----- 248  
Db 157 -----GPGAGDGTDPVHRGYLSVLTSEDQSELMKQSAARMQNKLG 199  
Qy 249 -----LOTKQLQMLTKTKDSTLTFAGHSGLATLSVSAFDIYEN----- 289  
Db 200 DPMRQTLKKVLTETARLMDKTKDEBTSITVIGHSIGATLATLANADIAANSYNGSSRD 259  
Qy 290 LTTEIPTAVAVFGCPKGVNKKFQQLPDSYRNVLAVHVRNVIDLRPLPVKLMGVNIGIB 349
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Db 260 LQACTPTAVAVFGSPRTGDRGFRDAFHLRLDLRLVNRNBPDRIPHPY--VGYADVGE 317  
Qy 350 LEIDSRKSTFLDSKSNPDMHNALQALIHVSGWHGVKGEFKVYNKRSVALVYNKSCDFLKE 409  
Db 318 LLDITRLSPFLRRGSSQSHDLECHLHGVAWGDHRRGELVVDROVALVKNKPDCLAD 377  
Qy 410 ECLVPPAMVVONKGMVNLKQGEVVLAPPEEDPTEPD 447  
Db 378 EYVPVVRNKKVHNKSMKVGPDGRWVLQDHEDDDDDDD 415
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RESULT 15
US-10-425-115-205760
; Sequence 205760, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 205760
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_119237C.1.pcp
US-10-425-115-205760

Query Match 30.3%; Score 721.5; DB 4; Length 430;
Best Local Similarity 36.6%; Pred. No. 7.1e-60;
Matches 164; Conservative 61; Mismatches 168; Indels 55; Gaps 7;

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Qy 3 AEAQPLGSKRPGPTWPELLGSNAGLNPINDELRELLRCGDFCQVYDTFINDONSS 62  
Db 23 AAQSQSQSQSQSQSMALSGRDWMDGLDPLDGRRAVIRYGLAQATSDAFIGDPA 82  
Qy 63 YCGSSRYGKADLLHKTFPGGADRFVVAIYATKAVSYPEAFLKSRSEKDRSNMIG 122  
Db 83 YAGASRYAPGAFLLRAQAP-DPDYVNTFRPLVATSSARVFGQFTTRPAPGASAESNM 141  
Qy 123 GYVVSNDETSRVAGREYVYVWRGCRDYEVDVGAQLESAPHLRTQOTTHVEKVEN 182  
Db 142 GYVAVADAGVARRGRDIIYVARRGTGRAVEMNDL----- 177  
Qy 183 BEKKSJHKSWMYDCFNINILGSASKDKGSDDDDDPKVMQGMNTYTSSEDPKSPFTK 242  
Db 178 -----DITLVPA-----GVVGPQGWQCPVHRGFLSVYASRNSTSRFNK 218  
Qy 243 LSAATQQLTKLQMLTKYKDELTSTFAGHSGLATLSVSAFDIYEN-----LTTEIP 295  
Db 219 KSAQOVLAIRIRRLDVIYKNCSTLTGHSIGALSTLNAIDIVANGLVNRCNDTVP 278  
Qy 296 VTAIVFGCPKGVNKKFQQLPDSYRNVLAVHVRNVIDLRPLPVKLMGVNIGLEIDSR 355  
Db 279 VAAIVFGSPRGDQFKCAFDLSAPGARLLVRNAPDVVPTVLPAAF--YKOVGVLLDTR 337  
Qy 356 KSTFLK--DSKQPSDMHNLQALIHVSGWHGV--KGEFKVYNKRSVALVYNKSCDFLKE 412  
Db 338 KSPHLKRPQGPAPAMHNLGECYLGAGTQAGDAAGFSLVDBDVALVNRKVALSDY 397  
Qy 413 VPPAMVVONKGMVNLKQGEVVLAPPEE 440  
Db 398 VPAAMVVEGKGMTRDASGRWVLQDHHE 425
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Search completed: December 22, 2005, 19:52:53
Job time : 114.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 22, 2005, 19:33:42 ; Search time 32.5 Seconds

(without alignments)
1137.109 Million cell updates/sec

Title: US-10-674-540A-2

Perfect score: 2385

Sequence: 1 MAEAQPLGSKPGPTWPEL.....NKDEWYAPREDPTPEFD 447

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: .572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodaca/1/1aa/5 COMB.pep:*

2: /cgn2_6/ptodaca/1/1aa/6 COMB.pep:*

3: /cgn2_6/ptodaca/1/1aa/H.COMB.pep:*

4: /cgn2_6/ptodaca/1/1aa/PTUS.COMB.pep:*

5: /cgn2_6/ptodaca/1/1aa/RE.COMB.pep:*

6: /cgn2_6/ptodaca/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2385	100.0	447	2	US-09-610-104C-2
2	2377	99.7	447	2	US-09-610-104C-11
3	1077	45.2	348	2	US-09-610-104C-16
4	775	32.5	418	2	US-09-610-104C-12
5	686.5	28.8	447	2	US-09-610-104C-19
6	684	28.7	448	2	US-09-610-104C-14
7	580.5	24.3	195	2	US-09-610-104C-17
8	576.5	24.2	401	2	US-09-610-104C-13
9	129.5	5.4	281	2	US-08-952-445-28
10	129.5	5.4	281	2	US-09-981-430-28
11	122.5	5.1	291	1	US-08-434-255-13
12	122.5	5.1	291	1	US-08-459-967-13
13	122.5	5.1	291	1	US-08-460-327-13
14	122.5	5.1	291	1	US-08-459-871-13
15	122.5	5.1	291	1	US-08-244-686-4
16	122.5	5.1	291	1	US-08-784-651-16
17	122.5	5.1	291	1	US-08-921-426-10
18	122.5	5.1	291	1	US-08-479-2750-2
19	122.5	5.1	291	1	US-08-488-2718-2
20	122.5	5.1	291	1	US-08-140-008A-2
21	122.5	5.1	291	1	US-08-701-339-2
22	122.5	5.1	291	1	US-08-816-915-10
23	122.5	5.1	291	2	US-09-024-532-6
24	122.5	5.1	291	2	US-09-007-288E-16
25	122.5	5.1	291	2	US-09-705-185-6
26	122.5	5.1	291	2	US-09-500-135C-227
27	122.5	5.1	291	2	US-09-768-080-227

28	122.5	5.1	291	2	US-09-677-822A-227	Sequence 227, App
29	122.5	5.1	291	4	PCT-US95-07743-10	Sequence 10, Appl
30	122.5	5.1	384	2	US-09-295-744A-14	Sequence 14, Appl
31	119.5	5.0	294	2	US-09-007-288E-142	Sequence 142, App
32	119.5	5.0	294	2	US-09-007-288E-143	Sequence 143, App
33	118.5	5.0	297	2	US-09-402-664A-9	Sequence 9, Appl
34	118.5	5.0	297	2	US-10-040-394-9	Sequence 9, Appl
35	117	4.9	130	2	US-09-434-840-33	Sequence 33, Appl
36	116.5	4.9	279	2	US-10-369-800-2	Sequence 2, Appl
37	115.5	4.8	297	1	US-08-859-106A-2	Sequence 2, Appl
38	110.5	4.6	130	2	US-09-434-840-32	Sequence 32, Appl
39	110.5	4.6	269	2	US-09-630-250B-19	Sequence 19, Appl
40	110.5	4.6	269	2	US-09-937-919-1	Sequence 1, Appl
41	110.5	4.6	270	2	US-08-362-525-8	Sequence 8, Appl
42	110.5	4.6	289	2	US-09-007-288E-145	Sequence 145, App
43	110.5	4.6	378	2	US-09-395-017B-1	Sequence 1, Appl
44	110.5	4.6	391	2	US-09-395-017B-2	Sequence 2, Appl
45	108	4.5	197	2	US-08-952-445-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1									
US-09-610-104C-2									
Sequence 2, Application US/09610104C									
Patent No. 6774284									
GENERAL INFORMATION:									
APPLICANT: John E. THOMPSON et al.									
TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,									
TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN									
FILE REFERENCE: 10799-10									
CURRENT APPLICATION NUMBER: US/09/610,104C									
CURRENT FILING DATE: 2000-07-05									
PRIOR APPLICATION NUMBER: 09/597,774									
PRIOR FILING DATE: 2000-06-09									
PRIOR APPLICATION NUMBER: 09/250,280									
PRIOR FILING DATE: 1999-02-16									
PRIOR APPLICATION NUMBER: 09/105,815									
PRIOR FILING DATE: 1998-06-26									
NUMBER OF SEQ ID NOS: 21									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 2									
LENGTH: 447									
TYPE: PRT									
ORGANISM: Plant									
US-09-610-104C-2									
Query Match									
Best Local Similarity 100.0%; Pred. No. 8.9e+28; Length 447;									
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MAEAQPLGSKPGPTWPEL	SGNAAGLPLNPLNDELRELLRCGDFCOVYDTFINDN	60					
DB	1	MAEAQPLGSKPGPTWPEL	SGNAAGLPLNPLNDELRELLRCGDFCOVYDTFINDN	60					
QY	61	SSYCGSSRYKADILHTTAPPGGADRPDYVAYATKAVSPEAFLLKSRREKWDRESN	120						
DB	61	SSYCGSSRYKADILHTTAPPGGADRPDYVAYATKAVSPEAFLLKSRREKWDRESN	120						
QY	121	WIGVVVSNDETSTVNAARRREVVVWMTGCRDYENVVVLGAOLSEAHPLRTOOTHYEV	180						
DB	121	WIGVVVSNDETSTVNAARRREVVVWMTGCRDYENVVVLGAOLSEAHPLRTOOTHYEV	180						
QY	181	ENEKKSIRHSSWYDCFNILGASAKDKGSGDDDDDDPKVQGMWITYTSEDPKS	240						
DB	181	ENEKKSIRHSSWYDCFNILGASAKDKGSGDDDDDDPKVQGMWITYTSEDPKS	240						
QY	241	TKLSARTLOTKLKQMLTKTKKDTLSTTPAGHSIGATLSVSAFDYENLTTEIPYNAV	300						
DB	241	TKLSARTLOTKLKQMLTKTKKDTLSTTPAGHSIGATLSVSAFDYENLTTEIPYNAV	300						

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Qy 301 FGCPCVGNKKFQQLFDSYPNLNLVLRNVLDLPLYPVKMGVYNGIELEIDSRKSTFL 360
|
Db 301 FGCPCVGNKKFQQLFDSYPNLNLVLRNVLDLPLYPVKMGVYNGIELEIDSRKSTFL 360
Qy 361 KDSKNPSDWMNLQAILHVSGMHWGKGFVKVNRKSVLVNKSDFLKECLVPPAMVV 420
|
Db 361 KDSKNPSDWMNLQAILHVSGMHWGKGFVKVNRKSVLVNKSDFLKECLVPPAMVV 420
Qy 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
|
Db 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
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RESULT 2

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US-09-610-104C-11
; Sequence 11, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 447
; TYPE: PRF
; ORGANISM: Plant
; US-09-610-104C-11
```

Query Match 99.7%; Score 2377; DB 2; Length 447;

Beet Local Similarity 99.8%; Pred. No. 6.4e-247; Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy 1 MAEAOPGLGSKPGTPPELGSNMAAGLNLNDELLELLRCDFQCVTYDFEINDQN 60
|
Db 1 MAEAOPGLGSKPGTPPELGSNMAAGLNLNDELLELLRCDFQCVTYDFEINDQN 60
Qy 61 SSYCGSSRYGKADLLHKTAFPGADRFDVVAIYATKAVSPEAFLLKSRSREKMDRESN 120
|
Db 61 SSYCGSSRYGKADLLHKTAFPGADRFDVVAIYATKAVSPEAFLLKSRSREKMDRESN 120
Qy 121 WIGYVVVSNDETSTRVAGREYVYVWRGTCRDYEWVDVGAQLESNHPILRTQOTTHVSKV 180
|
Db 121 WIGYVVVSNDETSTRVAGREYVYVWRGTCRDYEWVDVGAQLESNHPILRTQOTTHVSKV 180
Qy 181 ENEBKSTHKSWMYDCFNINLLGSASKDGKSDDDDDDDPKVMOGMMTIYTSBEDPKPF 240
|
Db 181 ENEBKSTHKSWMYDCFNINLLGSASKDGKSDDDDDDDPKVMOGMMTIYTSBEDPKPF 240
Qy 241 TKLSARLOQLTKLQMLTKYDETLSTFAGHSIGATLSVSAFDIVENLTTEIPVNAV 300
|
Db 241 TKLSARLOQLTKLQMLTKYDETLSTFAGHSIGATLSVSAFDIVENLTTEIPVNAV 300
Qy 301 FGCPCVGNKKFQQLFDSYPNLNLVLRNVLDLPLYPVKMGVYNGIELEIDSRKSTFL 360
|
Db 301 FGCPCVGNKKFQQLFDSYPNLNLVLRNVLDLPLYPVKMGVYNGIELEIDSRKSTFL 360
Qy 361 KDSKNPSDWMNLQAILHVSGMHWGKGFVKVNRKSVLVNKSDFLKECLVPPAMVV 420
|
Db 361 KDSKNPSDWMNLQAILHVSGMHWGKGFVKVNRKSVLVNKSDFLKECLVPPAMVV 420
Qy 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
|
Db 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447
```

Db 421 QNKGWVLNKDGEWVLAPPEEDPTPEFD 447

RESULT 3

```
US-09-610-104C-16
; Sequence 16, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 348
; TYPE: PRF
; ORGANISM: Plant
; US-09-610-104C-16
```

Query Match 45.2%; Score 1077; DB 2; Length 348;

Beet Local Similarity 55.2%; Pred. No. 5.1e-107; Matches 201; Conservative 63; Mismatches 74; Indels 26; Gaps 3;

```
Qy 84 ADREPVAVIYATKAVSPEAFLLKSRSREKMDRESNMGVYVNSDSTRVAGREYV 143
|
Db 10 ASDYEVNPLIYATKAVSPEAFLLKSRSREKMDRESNMGVYVNSDSTRVAGREYV 143
Qy 144 VWRGTCRDYEWVDVGAQLESNHPILRTQOTTHVSKVENEKSIHKSWMYDCFNINLLG 203
|
Db 70 ALRGTSHNYEWMVNLGAPTSADPLHGP-----EQDGGGVVGTTFD----- 113
Qy 204 SASDKKSGDDDDDDPKVMOGMMTIYTSBEDPKSTFKLSARLOQLTKLQMLTKYKDE 263
|
Db 114 -----SPSEBECCKMWLGWLTITYSNHPESKSTFKLSARLOQLTKLQMLTKYKDE 164
Qy 264 TLTSTFAGHSIGATLSVSAFDIVENLTTEIPVNAVFGCPKVGKPKFQQLFDSYPNLN 322
|
Db 165 KPSTIVLTGHSIGATLSVSAFDIVENLTTEIPVNAVFGCPKVGKPKFQQLFDSYPNLN 322
Qy 323 VLRNVNLDLPLYPVKMGVYNGIELEIDSRKSTFLKDSKNPSDWMNLQAILHVSGW 382
|
Db 225 ILHVRNLDLPLYPVKMGVYNGIELEIDSRKSTFLKDSKNPSDWMNLQAILHVSGW 284
Qy 383 HGVGKGFVKVNRKSVLVNKSDFLKECLVPPAMVVQNGWVLNKDGEWVLAPPEED 442
|
Db 285 NGKGEFELKWSRISALVNSCEFLKACLVPGSMWVEKNGKGLIKNEDEWVLAPPEED 344
Qy 443 TPEF 446
|
Db 345 VPEF 348
```

RESULT 4

```
US-09-610-104C-12
; Sequence 12, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
```

```

; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Plant
; US-09-610-104C-12

Query Match      32.5%; Score 775; DB 2; Length 418;
Best Local Similarity 37.5%; Pred. No. 2.4e-74;
Matches 167; Conservative 76; Mismatches 138; Indels 64; Gaps 9;

17 MPPELLGSNMAAGLNLPLNDELRELLRCGDFCQVTVDFINDONSYYCGSSRYGKADLLH 76
23 WRDLSGQNHMKMLQPLDQDLREYTHYGEWAQGYDTFNINTESQFAGASTYRKDPFA 82
77 KT-----AFPGADRFDVVAAYLYATAKVSYPEAFLLKSRSEKMDRESNMIGYVVSNDT 132
83 KVGLEIHP--YTKYKTKFIATSDIHVPESFLPISRGWGESNMWGYAVTDQ 140
133 SRVAGREVVYVWGTCRDYEWVDVLAQLESAPHLRTQOTTVEKYENEKKSIIKSS 192
141 TALGRRDIAIAMRGTVKLEIMADLKDYLRV-----TENKIR----- 175
193 WYDFENINLGSASAKDKKSGDDDDDDPKYMGGMNTIYSEDPKSPPTKLSARTOLTK 252
174 -----IKIRG-----ERNDQVQIHQGMSTYMSQDRSPPTKLNADQVLR 215
253 LKQMTKYKDETLITFAGHSLGATLSVSAFDIVE-----LTTELPTAVVFGCP 304
216 VGRLEKTKQBEVSIITCGHSLGALATDSALDIVANGVNRPKSRPKSCPTVAFVASF 275
305 KVGKKFQQLFDSYPLNLVHVRNVIDLIPLYPVKLMGYNIGIELIDSKSTFLKDSK 364
276 RVGSDPRKLFSGLEDIRVLRTRMLFDVIPPIYP--IGYSVGDPEPIDTRKSPYMKSPG 333
365 NPSMHLQALIHVSGMHV--KGE--FRVYNKRSVALVNSCDLKECVLPPAMVYON 422
334 NLATFHLEGYLHGVAGTQGTNKADLRLDVERAIGLVNKSVDGLKQECWPGKRVLYKN 393
423 KGMVLRKGWVLAAPREEDPTPEFD 447
394 KG-AQDDGSWEVLVDHEIDNEDLD 417

RESULT 5
US-09-610-104C-19
; Sequence 19, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; US-09-610-104C-19
```

```

; LENGTH: 447
; TYPE: PRT
; ORGANISM: Plant
; US-09-610-104C-19

Query Match      28.8%; Score 686.5; DB 2; Length 447;
Best Local Similarity 35.6%; Pred. No. 9.2e-65;
Matches 160; Conservative 78; Mismatches 133; Indels 79; Gaps 14;

16 TWPELLGSNMAAGLNLPLNDELRELLRCGDFCQVTVDFINDONSYYCGSSRYGKADLL 75
22 TWKRIQGEDWAGLMDMDPLRLSELIRYGEWAQACTADFPDPAKTCGTSRTLRLEFF 81
76 HKTAFPGADR--FDVVAAYLYATAKVSYPEAFLLKSRSEKMDRESNMIGYVVSNDTSR 134
82 DSL---GMDSGYEVARYLYATISNINPN--FPGSRKRSKYSKNAMMGVVAASDDTSR 137
135 -VAGREVVYVWGTCRDYEWVDVLAQLESAPHLRTQOTTVEKYENEKKSIIKSSW 193
138 NRLGRRDIAIAMRGTVKLEIMADLKDYLRV-----TENKIR----- 175
194 YDFENINLGSASAKDKKSGDDDDDDPKYMGGMNTIYSEDPKSPPTKLSARTOLTKL 253
176 --C-----PDPAVKVSGFLDYDKDTTCKFAFSAEQILREV 213
254 KQMTKYKDE---TLSTFAGHSLGATLSVSAFDIVE---NLTE---IPVAVFGCP 304
214 KRLVEHGGDDDDSLITTVGHSLGALATLSAVDIAEMKLNSKKGKVPVLYLVYGGP 273
305 KVGKKFQQLFDSYPLNLVHVRNVIDLIPLYPVKLMG-----YVNIQ 347
274 RVGNVRFRERMEEL--GVKVRVNVVHVDVPSGLFLNBSRPHALMKIAGLPWCYSHVG 332
348 IELEIDRSKSTFLKDSKRPDWHNLQALIHVSGMHVKE--FRVYNKRSVALVNSCDF 406
333 EELALDHQNSPFLKPSVDVSTAHNLEMLHLDSYHG--KGEFVLSGDRHALVNRKASDF 391
407 LKEECVLPAMVYVONKGMVLRKGWVLA 436
392 LKEHLQIPFWRQDANKGMVRNSGRWIOA 421

RESULT 6
US-09-610-104C-14
; Sequence 14, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; CURRENT FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Plant
; US-09-610-104C-14

Query Match      28.7%; Score 684; DB 2; Length 448;
Best Local Similarity 35.9%; Pred. No. 1.7e-64;
Matches 162; Conservative 78; Mismatches 131; Indels 80; Gaps 15;

16 TWPELLGSNMAAGLNLPLNDELRELLRCGDFCQVTVDFINDONSYYCGSSRYGKADLL 75
```

```
Db 22 TWRKIQGGDDWAGLMDPMDPIIRSELIRYGEWAQACYPAFDFDPASKYCGTSRFRLEFF 81
Qy 76 HKTAFPGGADR-FDVVAATYATKAVSVEAFLLKRSRREKMDREBNWIGYVVSNDERSR 134
Db 82 DSL---GNTDSGYEARLYATISNINLPN-FPSKSRMSKWSKMANMGIVAVSDDETSR 137
Qy 135 -VAGREYVYVWRCGRDYEMWDLGAQLESAPLIRTOQTHVEKVENEEKSIHKSWS 193
Db 138 NRLGRDIAIMRGVTUTLEWIMADKDYLPV-----TENKIR----- 175
Qy 194 YDCFNINILSGASKDGSGDDDDDDPRKMGMMTIYTSDEPKSPFTKLSARTOLOTKL 253
Db 176 --C-----PPPAKVESGFDLTYDXTCKFARFASRBEQILREV 213
Qy 254 KQIMTKYKDE---TLSTFAGHSIGATLSVVSAPFIVE---NLJTE---IPYAVV-FGC 303
Db 214 KRLVEHGGDDSDSLSTVTGSHLGALAILSAIDAEMLNRSKKGKVIPTAVLYIGG 273
Qy 304 PKVGKKKFOQLFDSYPNILVHVRNVIDLPLYPVKLNG-----YVNI 346
Db 274 PRGVVRREMEEL-GYKVRVYVHVDPKSPGLFLESRPHAMKIASGLPWCYSHV 332
Qy 347 GIELEIDRSKSTFLKDSKNPSDMNLQAILHVSGMHGKGE-FKVNKRSVALYVNSCD 405
Db 333 GEEELADHQNSPFLKPSYDVSTAHNLLEAMHLDDYHG-KGERFVLSGRDHALVYKASD 391
Qy 406 FLKEECVLPAMVWVQNGMYLNDGGEVLA 436
Db 392 FLKEHLQIPFPRDANKGVANSSEGRWIOA 422
```

RESULT 7

```
US-09-610-104C-17
; Sequence 17, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE,
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Plant
US-09-610-104C-17
```

```
Query Match 24.3%; Score 580.5; DB 2; Length 195;
Best Local Similarity 53.4%; Pred. No. 6,1e-54;
Matches 119; Conservative 31; Mismatches 44; Indels 29; Gaps 4;

Qy 151 DYEMWDVLAGQLESAPLIRTOQTHVEKVENEEKSIHKSWSYCPNINILSGASKDG 210
Db 1 DYEMWDVLAGRDSDSL-----HPKSLCK-----GIN-----NKN 32
Qy 211 KGSDDDDDDPKVMGMMTIYTSDEPKSPFTKLSARTOLOTKLQIMTKYKDETLSTFPA 270
Db 33 DEDDEDEDEIKVMGMLKTIYVSNPKSFTRLSAREQOAIETKLRNEYKDENLSTFT 92
Qy 271 GHSIGATLSVVSAPFIVEN-LTTEIPYAVVFGCPVGKPKFQQLFDSYPNILVHVRNV 329
Db 93 GHSIGATLSVVSAPFIVEN-LTTEIPYAVVFGCPVGKPKFQQLFDSYPNILVHVRNV 152
```

```
Qy 330 IDLILPYVXKMGYVNIIGIELEIDRSKSTFLKDSKNPSDMNL 372
Db 153 IDLITLYPSALFGYVNSGIELEIDRSKSPSLKDSKMDGMHNL 195
```

RESULT 8

```
US-09-610-104C-13
; Sequence 13, Application US/09610104C
; Patent No. 6774284
; GENERAL INFORMATION:
; APPLICANT: John E. THOMPSON et al.
; TITLE OF INVENTION: DNA ENCODING A PLANT LIPASE.
; TITLE OF INVENTION: TRANSGENIC PLANTS AND A METHOD FOR CONTROLLING SENESENCE IN
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 10799-10
; CURRENT APPLICATION NUMBER: US/09/610,104C
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: 09/597,774
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 09/250,280
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 09/105,815
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Plant
US-09-610-104C-13
```

```
Query Match 24.2%; Score 576.5; DB 2; Length 401;
Best Local Similarity 30.8%; Pred. No. 5.5e-53;
Matches 138; Conservative 79; Mismatches 168; Indels 63; Gaps 8;
```

```
Qy 9 GLSRPGTWPBELLGSSNAGLNLNDELRLRCDFCQVYDTITINDONSSYCGSSR 68
Db 3 GIAR---RMKVLSSGDWEGLEBLDRLRYLHYGTWVSPATDSFINEMASRKNVGLPR 59
Qy 69 YGRKDLHKTRAF-FGADRPRVVAATKAVSP-EAFLKRSRREKMDREBNWIGYV 126
Db 60 YARNNLNLCGLVKNPDKIEVITYFA PSTIPLDGYNVRATRADAVLKESMNGYVA 119
Qy 127 VSNDETSVAGRREYVWRCGRDYEMWDLGAQLESAPLIRTOQTHVEKVENEEK 186
Db 120 VATDEGVALGRDILLYVMGTIRKSEMNEULTFWFKYA-PLPFGQ----- 164
Qy 187 SIHSSWYDCFNINILSGASKDGSGDDDDDDPKVMGMMTIYTSDEPKSPFTKLSAR 246
Db 165 -----NSDPLVHKGYDWTYITINDOSQLNEKSAR 193
Qy 247 TLOLTKLQIMTKYKDETLSTFAGHSIGATLSVVSAPFIVE---NLJTEIPYAVVFGC 303
Db 194 DQIREVARLVELYKDEISTVTGSHLGSSMATLNVDLAANDINNKNILVTAFLYAS 253
Qy 304 PKVGKKKFOQLFDSYPNILVHVRNVIDLPLYPV-----KLMGYVNIIGIELEIDSR 355
Db 254 PKVGDENKVIVISNOQILRALRISDVNDIYAVVFPFGKCECDNALIYGDVGGLVIDSK 313
Qy 356 KSTFLKDSKNPSDMNLQAILHVSGMHGKGEKRVVNSKVALYVNSCDFLKEECVLP 415
Db 314 KSHYLPKDFPRLSTHDLMLYHAIIDGYOGSGGGEFQEDFDLAKVKKGYDLKAEYPIPI 373
Qy 416 AMWVWVQNGMYLNDGGEVLAAPPEDFP 443
Db 374 GWFNIKDKGM-QQDDGNYITLDHDEVDT 400
```

RESULT 9

```
US-08-952-445-28
; Sequence 28, Application US/08952445
; Patent No. 6368833
```


GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: ESTERASE ENZYMES, DNA ENCODING
TITLE OF INVENTION: ESTERASE ENZYMES AND VECTORS AND HOST CELLS INCORPORATING SAME
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,445
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/722,713
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC362-2-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7555
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-952-445-28

Query Match 5.4%; Score 129.5; DB 2; Length 281;
Best Local Similarity 24.6%; Pred. No. 4.4e-05;
Matches 64; Conservative 38; Mismatches 81; Indels 77; Gaps 12;

157 VLAQLESAHPLRTQOTTHVEKEN-EKKSIHKSWMYCFNIN----- 200
9 VLAVVVAGHALAASSTGISEDLSRLVENATISQAAYADLCNIPSTTIKGEKTYNSQTD 68
201 -----LIGSASKD-----KKGSGDDDDDDPKVMQGMWITYTSEDPKSPFTKL----- 243
69 INGMILRDDSKEIITVFRGTGSDTNQLD-----TNYT-----LTPDPTLPQNGCE 116
244 -----SARTQLOTKLKQMTKYKDETLSTTFAGHSIGATLSVVSAPDIVENLTTB 293
117 VHGGYIIGWVSVDQVESLVKQOVQYPDVALTVT--GHSIGASIALTAOL---SATY 171
294 IPTAVAVGCPKVGKFKFOOLFDSYPN-----LNVLHVRNVIDLPLVPVKLMGY 343
172 DNIIRLYTFGEPRSGN---QAFASYMDADFQASSPDTTQYFRVTHANDGILPNLPVEQGY 227

344 VNIGIEL-EID--SRKSTFL 360
228 AHGVEYWSVDPPYSAQNTFV 247

RESULT 10
US-09-981-430-28
Sequence 28, Application US/09981430
Patent No. 6828136
GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: ESTERASE ENZYMES, DNA ENCODING
ESTERASE ENZYMES AND VECTORS AND HOST CELLS INCORPORATING S
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genencor International, Inc.
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/981,430
FILING DATE: 15-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/952,445
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC362-2-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7555
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-981-430-28

Query Match 5.4%; Score 129.5; DB 2; Length 281;
Best Local Similarity 24.6%; Pred. No. 4.4e-05;
Matches 64; Conservative 38; Mismatches 81; Indels 77; Gaps 12;

157 VLAQLESAHPLRTQOTTHVEKEN-EKKSIHKSWMYCFNIN----- 200
9 VLAVVVAGHALAASSTGISEDLSRLVENATISQAAYADLCNIPSTTIKGEKTYNSQTD 68
201 -----LIGSASKD-----KKGSGDDDDDDPKVMQGMWITYTSEDPKSPFTKL----- 243
69 INGMILRDDSKEIITVFRGTGSDTNQLD-----TNYT-----LTPDPTLPQNGCE 116
244 -----SARTQLOTKLKQMTKYKDETLSTTFAGHSIGATLSVVSAPDIVENLTTB 293
117 VHGGYIIGWVSVDQVESLVKQOVQYPDVALTVT--GHSIGASIALTAOL---SATY 171
294 IPTAVAVGCPKVGKFKFOOLFDSYPN-----LNVLHVRNVIDLPLVPVKLMGY 343
172 DNIIRLYTFGEPRSGN---QAFASYMDADFQASSPDTTQYFRVTHANDGILPNLPVEQGY 227

344 VNIGIEL-EID--SRKSTFL 360
228 AHGVEYWSVDPPYSAQNTFV 247

RESULT 11
US-08-434-255-13
Sequence 13, Application US/08434255
Patent No. 5621089
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dammann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5621089 No. 5621089disk of No. 5621089th America, Inc.
STREET: 405 Lexington Avenue, 64th floor
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agilis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764,400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-434-255-13

Query Match 5.1%; Score 122.5; DB 1; Length 291;

Best Local Similarity 17.7%; Pred. No. 0.00027; Indels 99; Gaps 12;
Matches 59; Conservative 55; Mismatches 120;

24 NAMAGLPLNDELRELLRCGDFCQVYDTPFINDQNSYCGSSRYGKADLLHKTAFPGG 83
11 SAMTALSPTRREVSQLFN-----QENLFAQYSAACGKNDA-----PAG 53
84 ADFPDVAAYLYATAKVSPPEAFILKSRREKMDRESNMGIVV--VSNDETSRVAGREV 141
54 T---NITCTGNAACEVEKADATFL-----YSFEDSGVGDVTCFLALDNTNKL-----I 98
142 YVWAGTCRDYEWVDVYGAQLESAPHLRTQOOTHVEKVENBEKKS IHKSSWYDGFNINL 201
99 VLSFRGSRSIENWIGNLN-----FDLKEIND 124
202 LGSASKDKGSGDDDDDDPKVMQGMITYSEDPKSPFTKLARTQLOTKLQMLTKYK 261
125 ICSGC---RGHDG-----FTSMRSVADT-----LRQKVEDAVREHP 158
262 DETLSITFAGSLGATLSVSAFDIVENLTTEIPVTAVVFGCPKVGKKFQQLFDSYPNL 321
159 D--YRVVFTGSHLGALATVAGADLRGN---GYDIDVFSYGAPRVGNRAFAEFLTVQTGG 213
322 NVLHVRNVIDLPIYPVKLMGYVNIIGIELEIDS 354
214 TLVRIHTNDIVPRLPRREFGYSHSSPEYWIKS 246

RESULT 12

US-08-459-967-13

Sequence 13, Application US/08459967

Patent No. 5622841

GENERAL INFORMATION:

APPLICANT: Sloma, Alan P.

APPLICANT: Outtrup, Heile

APPLICANT: Dammann, Claus

APPLICANT: Aaslyng, Dorrit

TITLE OF INVENTION: ALKALINE PROTEASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 56228410 No. 5622841disk of No. 5622841th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,967
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,255
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Agilis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764,400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-967-13

Query Match 5.1%; Score 122.5; DB 1; Length 291;

Best Local Similarity 17.7%; Pred. No. 0.00027; Indels 99; Gaps 12;
Matches 59; Conservative 55; Mismatches 120;

24 NAMAGLPLNDELRELLRCGDFCQVYDTPFINDQNSYCGSSRYGKADLLHKTAFPGG 83
11 SAMTALSPTRREVSQLFN-----QENLFAQYSAACGKNDA-----PAG 53
84 ADFPDVAAYLYATAKVSPPEAFILKSRREKMDRESNMGIVV--VSNDETSRVAGREV 141
54 T---NITCTGNAACEVEKADATFL-----YSFEDSGVGDVTCFLALDNTNKL-----I 98
142 YVWAGTCRDYEWVDVYGAQLESAPHLRTQOOTHVEKVENBEKKS IHKSSWYDGFNINL 201
99 VLSFRGSRSIENWIGNLN-----FDLKEIND 124
202 LGSASKDKGSGDDDDDDPKVMQGMITYSEDPKSPFTKLARTQLOTKLQMLTKYK 261
125 ICSGC---RGHDG-----FTSMRSVADT-----LRQKVEDAVREHP 158
262 DETLSITFAGSLGATLSVSAFDIVENLTTEIPVTAVVFGCPKVGKKFQQLFDSYPNL 321
159 D--YRVVFTGSHLGALATVAGADLRGN---GYDIDVFSYGAPRVGNRAFAEFLTVQTGG 213
322 NVLHVRNVIDLPIYPVKLMGYVNIIGIELEIDS 354
214 TLVRIHTNDIVPRLPRREFGYSHSSPEYWIKS 246

RESULT 13

US-08-460-327-13

Sequence 13, Application US/08460327

Patent No. 5622850

GENERAL INFORMATION:

APPLICANT: Sloma, Alan P.

APPLICANT: Outtrup, Heile

APPLICANT: Dammann, Claus

APPLICANT: Aaslyng, Dorrit

TITLE OF INVENTION: ALKALINE PROTEASE

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 56228500 No. 5622850disk of No. 5622850th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,327
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,255
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Agilis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764,400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-327-13

Query Match 5.1%; Score 122.5; DB 1; Length 291;
Best Local Similarity 17.7%; Pred. No. 0.00027;
Matches 59; Conservative 55; Mismatches 120; Indels 99; Gaps 12;

QY 24 NAWAGLPLNDELRLRLRCGDFCQVYTFINDNSSYCGSSRYGKADLHKTAPGG 83
DB 11 SAWTALASPIRREVSOQLFN-----QFNLFAGYSAAYCGKNDA-----PAG 53
QY 84 ADRPDVAVIYATKAVPEAFLLKSRREKMDRESNIGYV--VNDSTSRVAGREV 141
DB 54 T--NITCTGNACPEVEKADATFL-----YSPEDSGVDYGVFLALDNTNKL-----I 98
QY 142 YVWRGTCRDYEWVVDVLAQLESAPLLRTQOTTHVEKVENEEKSIHKSMDYCFNINL 201
DB 99 VLSFRGSRSLIENMIGNLN-----FTSSWRSVADT-----LRQVEDAVREHP 158
QY 202 LGSASDKGKSGDDDDDDPKVMQGMWTIYTSBDPKSPFTKLSARLOQLTKQLMTKTKYK 261
DB 125 ICSGC-----RGHDG-----FTSSWRSVADT-----LRQVEDAVREHP 158
QY 262 DETLSITFAGHSIGATLSVVSAPDIYENLTTEIPVTAIVFGCPKVGKKTKOQLFDSYPNL 321
DB 159 D--YRVVFTHSGSLGALATVAGADLRGN--GYDIDVFSYGAPRVGRAPAEFLTVQTGG 213
QY 322 NVLHVRNVLDILPLYPKLMGVNIGIELEIDS 354
DB 214 TVYRITHNDIVPLPREFFGYSHSPEYTIKS 246

RESULT 14
US-08-459-871-13
Sequence 13, Application US/08459871
Patent No. 5650326
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Heile
APPLICANT: Dammann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5650326 No. 5650326 disk of No. 5650326th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,871
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,255
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Agilis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764,400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-871-13

Query Match 5.1%; Score 122.5; DB 1; Length 291;
Best Local Similarity 17.7%; Pred. No. 0.00027;
Matches 59; Conservative 55; Mismatches 120; Indels 99; Gaps 12;

QY 24 NAWAGLPLNDELRLRLRCGDFCQVYTFINDNSSYCGSSRYGKADLHKTAPGG 83
DB 11 SAWTALASPIRREVSOQLFN-----QFNLFAGYSAAYCGKNDA-----PAG 53
QY 84 ADRPDVAVIYATKAVPEAFLLKSRREKMDRESNIGYV--VNDSTSRVAGREV 141
DB 54 T--NITCTGNACPEVEKADATFL-----YSPEDSGVDYGVFLALDNTNKL-----I 98
QY 142 YVWRGTCRDYEWVVDVLAQLESAPLLRTQOTTHVEKVENEEKSIHKSMDYCFNINL 201
DB 99 VLSFRGSRSLIENMIGNLN-----FTSSWRSVADT-----LRQVEDAVREHP 158
QY 202 LGSASDKGKSGDDDDDDPKVMQGMWTIYTSBDPKSPFTKLSARLOQLTKQLMTKTKYK 261
DB 125 ICSGC-----RGHDG-----FTSSWRSVADT-----LRQVEDAVREHP 158
QY 262 DETLSITFAGHSIGATLSVVSAPDIYENLTTEIPVTAIVFGCPKVGKKTKOQLFDSYPNL 321
DB 159 D--YRVVFTHSGSLGALATVAGADLRGN--GYDIDVFSYGAPRVGRAPAEFLTVQTGG 213
QY 322 NVLHVRNVLDILPLYPKLMGVNIGIELEIDS 354
DB 214 TVYRITHNDIVPLPREFFGYSHSPEYTIKS 246

RESULT 15
US-08-244-686-4
Sequence 4, Application US/08244686
Patent No. 5705358
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Process for the production of a protein
TITLE OF INVENTION: using endoxylanase II (exIIa) expression signals
NUMBER OF SEQUENCES: 12
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,686
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-244-686-4

Query Match 5.1%; Score 122.5; DB 1; Length 291;
Best Local Similarity 17.7%; Pred. No. 0.00027;
Matches 59; Conservative 55; Mismatches 120; Indels 99; Gaps 12;

QY 24 NAMAGLNPDELRLRCGDPQVYDTFINDQNSYCGSSRYGKADLLHKTAPFG 83
DB 11 SAWTALASPIRREVSDLEFN-----QFNLPAGYSAAYCGKNDA-----PAG 53
QY 84 ADREPVVAVYATAKVSVPEAFLLKSRSEKMDRESNMIGYV--VSNDETSRVAGRREV 141
DB 54 T---NITCTGNAQCEVEKADATFL-----YSPEDSGVDVTGFLADNTNKL-----I 98
QY 142 YVVRGTCRDYEWVDVGAQLSAHPLRTQOTTHVEKENEKKSIIKSSWYDCFNINL 201
DB 99 VLSFRGSRSEIENWIGNLN-----FDLKEIND 124
QY 202 LGSASXDKGSGSDDDDDPKVMGQMWITYSDEPKSPFTKLARSATOLQTLKQUMTKYK 261
DB 125 ICSGC---RGHDG-----FTSWMRSVADT-----LROKVEDAVREHP 158
QY 262 DETLSITPAGSLGATLSVSAFDIVENLTTEIPVTAVVFGCPKVGKKFOOLFDSYPNL 321
DB 159 D--YRVVFTGSHLGALATVAGADIRGN---GYDIDVFSYGAPRYGNRAFAEFLVTGTG 213
QY 322 NVLHVRNVIDLPLYPVKLMGYVNIIGLEIDS 354
DB 214 TLVRIHTNDIVPRLPRRFGYSHSSPEYWIKS 246

Search completed: December 22, 2005, 19:49:01
Job time : 34.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 22, 2005, 19:33:07 ; Search time 131.5 Seconds
(without alignments)
1493.554 Million cell updates/sec

Title: US-10-674-540A-2
Perfect score: 2385
Sequence: 1 MAABAPQLGLSKPGPTWPEL.....NKDGEWTLAPPEEDPTPEFD 447

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*

1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*
9:	Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2385	100.0	447	3	AAV97298 Senescenc
2	2377	99.7	447	3	AAV97304 Senescenc
3	2377	99.7	447	5	AAU11997 Carnation
4	1311.5	55.0	412	3	AAG29751 Arabidops
5	1311.5	55.0	412	5	ABB92084 Arabidops
6	1311.5	55.0	412	8	ADU20619 Arabidops
7	1311.5	55.0	412	8	ADU20662 A. thalia
8	1311.5	55.0	418	3	AAAG29750 Arabidops
9	1082	45.4	343	3	AAAG29752 Arabidops
10	1077	45.2	348	5	AAV97308 Carnation
11	1077	44.2	348	5	AAU12003 Carnation
12	1054	44.2	510	7	ABM86048 Arabidops
13	824.5	34.6	410	8	ADY24723 Plant ful
14	789.5	33.1	419	5	ABM92980 Arabidops
15	775	32.5	418	3	AAV97305 Senescenc
16	770.5	32.3	423	5	ABB90874 Arabidops
17	767.5	32.2	423	3	AAAG28472 Arabidops
18	767.5	32.2	423	3	AAAG28472 Arabidops
19	767.5	32.2	423	8	ADT55973 Plant pol
20	767.5	32.2	438	3	AAAG28471 Arabidops
21	767.5	32.2	438	3	AAAG25411 Arabidops
22	766.5	32.1	423	3	AAAG27394 Arabidops
23	766.5	32.1	438	3	AAAG27393 Arabidops
24	766	32.1	434	8	ADT59706 Plant pol

25	725.5	30.4	358	7	ABM86264 Rice abio
26	705	29.6	434	8	ADX93643 Plant ful
27	705	29.6	515	8	ADX76485 Arabidops
28	691.5	29.0	385	3	AAAG25413 Arabidops
29	691.5	29.0	385	3	AAAG28473 Arabidops
30	690.5	29.0	385	3	AAAG27395 Arabidops
31	686.5	28.8	447	3	AAAG22257 Arabidops
32	686.5	28.8	447	3	AAAG45635 Arabidops
33	686.5	28.8	447	5	ABB91949 Arabidops
34	686.5	28.8	447	5	AAU12004 Arabidops
35	686.5	28.8	529	3	AAAG45634 Arabidops
36	686.5	28.8	529	3	AAAG22256 Arabidops
37	684	28.7	448	3	AAV97307 Senescenc
38	670	28.1	515	5	ABB90883 Arabidops
39	659	27.6	472	8	ADX78298 Plant ful
40	641.5	26.9	412	3	AAAG22258 Arabidops
41	641.5	26.9	412	3	AAAG45636 Arabidops
42	616	25.8	355	5	ABB91958 Arabidops
43	610.5	25.6	397	8	ADY08595 Plant ful
44	606.5	25.4	529	5	ABB91187 Arabidops
45	580.5	24.3	195	3	AAV97303 Senescenc

ALIGNMENTS

RESULT 1
AAV97298
ID AAV97298 standard; protein; 447 AA.
AC AAV97298;
XX
DT 03-JAN-2001 (first entry)
XX
DE Senescence-induced lipase.
XX
KW Senescence-induced lipase; senescence; lipase; antisense; regulation;
KW modulation; resistance; stress; crop protection; ethylene.
OS Dianthus caryophyllus.
XX
PN WO200049164-A1.
XX
PD 24-AUG-2000.
XX
PP 14-FEB-2000; 2000WO-US003494.
XX
PR 16-FEB-1999; 99US-00250280.
XX
PA (SENE-) SENESCO INC.
XX
FI Thompson JE, Wang T, Hudak K, Hong Y;
XX
DR WPI; 2000-549277/50.
XX
DR N-PSDB; AAAS3880.
XX
PT DNA encoding carnation senescence-induced lipase, useful for regulating
PT the expression of senescence in plants to delay its onset and improve
PT plant resistance to environmental stress, thus extending shelf-life or
PT growth period.
XX
PS Claim 5; Page 71-72; 89pp; English.
XX
XX Insertion of the senescence-induced lipase coding sequence in an
XX antisense direction in a plant genome can be used to regulate the
XX expression of senescence in those plants. Alteration of expression of the
XX senescence-induced lipase gene in plants results in delayed onset of
XX senescence and improved resistance to environmental stress, thus
XX extending the plant shelf-life and/or growth period. The genetically
XX altered plant is useful for producing a new variety or line of plants
XX where the alteration is stably transmitted from generation to generation.
XX This method of regulation is advantageous over prior senescence
XX modulating technologies since prior methods were only applicable to a

limited range of plants, e.g. to plants that are ethylene-sensitive. The antisense regulation method is applicable to all types of plants, regardless of ethylene sensitivity

Sequence 447 AA;

Query Match 100.0%; Score 2385; DB 3; Length 447;
Best Local Similarity 100.0%; Pred. No. 3.9e-234;
Matches 447; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MAAEAPLGLSKPGPTPELLGSNAAGLPLNDELRELLRCGDFCQVYDTFINDON 60
DB 1 MAAEAPLGLSKPGPTPELLGSNAAGLPLNDELRELLRCGDFCQVYDTFINDON 60
QY 61 SSYCGSSRYGKADLLHKTAFPGADRFVVAIYATAKVSVEAFLLKSRREKMDRESN 120
DB 61 SSYCGSSRYGKADLLHKTAFPGADRFVVAIYATAKVSVEAFLLKSRREKMDRESN 120
QY 121 WIGYVVSNDSTSRVAGREYVVMRGTCRDYEWVDVGAQLESAPLRTQOTTHVEKV 180
DB 121 WIGYVVSNDSTSRVAGREYVVMRGTCRDYEWVDVGAQLESAPLRTQOTTHVEKV 180
QY 181 ENEBKSIHKSQWYDCFNINILGSASKDKGSGDDDDDDPKVMQGMWTIYTSBDPKSPF 240
DB 181 ENEBKSIHKSQWYDCFNINILGSASKDKGSGDDDDDDPKVMQGMWTIYTSBDPKSPF 240
QY 241 TKLSARTQLQTKLQMLTKYDETLSTFAGHSIGATLSVSAPIVENLTTEIPVTAVV 300
DB 241 TKLSARTQLQTKLQMLTKYDETLSTFAGHSIGATLSVSAPIVENLTTEIPVTAVV 300
QY 301 FGCPVGNKKRQQLFDSYPNINLVHVRNVIDLPLYPVKLMGYNIGIELEIDSRKSTFL 360
DB 301 FGCPVGNKKRQQLFDSYPNINLVHVRNVIDLPLYPVKLMGYNIGIELEIDSRKSTFL 360
QY 361 KDSKNPDMHNLQAILHVVSGMHGKGFKVYVNRKSVLVNKSDFLKEBCLVPPAMVV 420
DB 361 KDSKNPDMHNLQAILHVVSGMHGKGFKVYVNRKSVLVNKSDFLKEBCLVPPAMVV 420
QY 421 QNKGWVLNKDEWVLAPPEEDPTPEFD 447
DB 421 QNKGWVLNKDEWVLAPPEEDPTPEFD 447

```

RESULT 2

AA197304 ID AA197304 standard; protein; 447 AA.

AA197304;

03-JAN-2001 (first entry)

Senescence-induced lipase (Car1ip).

Senescence-induced lipase; senescence; lipase; antisense; regulation; modulation; resistance; stress; crop protection; ethylene.

Dianthus caryophyllus.

WO20049164-A1.

24-AUG-2000.

14-FEB-2000; 2000WO-US003494.

16-FEB-1999; 99US-00250280.

(SENE-) SENESCO INC.

Thompson JB, Wang T, Hudak K, Hong Y;

WPI; 2000-549277/50.

DNA encoding carnation senescence-induced lipase, useful for regulating

the expression of senescence in plants to delay its onset and improve plant resistance to environmental stress, thus extending shelf-life or growth period.

Disclosure; Page 75-76; 89pp; English.

Insertion of the senescence-induced lipase coding sequence in an antisense direction in a plant genome can be used to regulate the expression of senescence in those plants. Alteration of expression of the senescence-induced lipase gene in plants results in delayed onset of senescence and improved resistance to environmental stress, thus extending the plant shelf-life and/or growth period. The genetically altered plant is useful for producing a new variety or line of plants where the alteration is stably transmitted from generation to generation. This method of regulation is advantageous over prior senescence modulating technologies since prior methods were only applicable to a limited range of plants, e.g. to plants that are ethylene-sensitive. The antisense regulation method is applicable to all types of plants, regardless of ethylene sensitivity

Sequence 447 AA;

Query Match 99.7%; Score 2377; DB 3; Length 447;
Best Local Similarity 99.8%; Pred. No. 2.6e-233;
Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 MAAEAPLGLSKPGPTPELLGSNAAGLPLNDELRELLRCGDFCQVYDTFINDON 60
DB 1 MAAEAPLGLSKPGPTPELLGSNAAGLPLNDELRELLRCGDFCQVYDTFINDON 60
QY 61 SSYCGSSRYGKADLLHKTAFPGADRFVVAIYATAKVSVEAFLLKSRREKMDRESN 120
DB 61 SSYCGSSRYGKADLLHKTAFPGADRFVVAIYATAKVSVEAFLLKSRREKMDRESN 120
QY 121 WIGYVVSNDSTSRVAGREYVVMRGTCRDYEWVDVGAQLESAPLRTQOTTHVEKV 180
DB 121 WIGYVVSNDSTSRVAGREYVVMRGTCRDYEWVDVGAQLESAPLRTQOTTHVEKV 180
QY 181 ENEBKSIHKSQWYDCFNINILGSASKDKGSGDDDDDDPKVMQGMWTIYTSBDPKSPF 240
DB 181 ENEBKSIHKSQWYDCFNINILGSASKDKGSGDDDDDDPKVMQGMWTIYTSBDPKSPF 240
QY 241 TKLSARTQLQTKLQMLTKYDETLSTFAGHSIGATLSVSAPIVENLTTEIPVTAVV 300
DB 241 TKLSARTQLQTKLQMLTKYDETLSTFAGHSIGATLSVSAPIVENLTTEIPVTAVV 300
QY 301 FGCPVGNKKRQQLFDSYPNINLVHVRNVIDLPLYPVKLMGYNIGIELEIDSRKSTFL 360
DB 301 FGCPVGNKKRQQLFDSYPNINLVHVRNVIDLPLYPVKLMGYNIGIELEIDSRKSTFL 360
QY 361 KDSKNPDMHNLQAILHVVSGMHGKGFKVYVNRKSVLVNKSDFLKEBCLVPPAMVV 420
DB 361 KDSKNPDMHNLQAILHVVSGMHGKGFKVYVNRKSVLVNKSDFLKEBCLVPPAMVV 420
QY 421 QNKGWVLNKDEWVLAPPEEDPTPEFD 447
DB 421 QNKGWVLNKDEWVLAPPEEDPTPEFD 447

```

RESULT 3

AAU11997 ID AAU11997 standard; protein; 447 AA.

AAU11997;

09-APR-2002 (first entry)

Carnation senescence-induced lipase.

Plant; senescence-induced lipase; regulation of senescence; environmental stress; carnation; enzyme.

Dianthus caryophyllus.

XX	Key	Location/Qualifiers
FR	Misc-difference	70
FT	/note= "Encoded by GCG"	
XX	MO200198510-A2.	
XX	19-JUN-2001; 2001WO-US019385.	
XX	27-DEC-2001.	
PD	19-JUN-2001; 2001WO-US019385.	
XX	19-JUN-2000; 2000US-00597774.	
PR	05-JUL-2000; 2000US-00610104.	
XX	(SENE-) SENESCO TECHNOLOGIES INC.	
PA	Thompson JE, Wang T, Hudak K, Hong Y;	
XX	WPI: 2002-130793/17.	
DR	N-PSDB; AAS20751.	
XX	New carnation and Arabidopsis genes encoding a senescence-induced lipase,	
PT	useful for controlling (onset of) senescence in plants, regulating	
PT	expression of senescence in plants, or modifying senescence in transgenic	
PT	plants.	
XX	Claim 6; Fig 1; 106pp; English.	
PS	The present invention relates to the isolation of polynucleotide	
XX	sequences encoding plant (carnation and Arabidopsis) senescence-induced	
CC	lipases. Regulation of expression of senescence in plants is obtained by	
CC	integration of a gene or gene fragment encoding senescence-induced lipase	
CC	into the plant genome. The isolated polynucleotide sequences are useful	
CC	for controlling senescence or the onset of senescence in plants caused by	
CC	either internal or external factors (e.g. environmental stress), or	
CC	regulating expression of senescence in plants. The DNAs are also useful	
CC	for modifying senescence in transgenic plants. The present sequence	
CC	represents carnation senescence-induced lipase	
XX	Sequence 447 AA;	
XX	Query Match 99.7%; Score 2377; DB 5; Length 447;	
XX	Best Local Similarity 99.8%; Pred. No. 2.6e-233;	
XX	Matches 446; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
QY	1 MAEAPQPIGLSKPGETTBELIGSNAMAGLNLPLNDELRELRLRCGDFCVYTDPIINDON 60	
DB	1 MAEAPQPIGLSKPGETTBELIGSNAMAGLNLPLNDELRELRLRCGDFCVYTDPIINDON 60	
QY	61 SSYGSSSYGKADLLHKTAPFGAGAPFDVAALVYATAKSVSEAFILKRSREKMDREN 120	
DB	61 SSYGSSSYGKADLLHKTAPFGAGAPFDVAALVYATAKSVSEAFILKRSREKMDREN 120	
QY	121 WIGYVVENDETSRVARGRREVYVWVRGTCRDYEWYDVLAGQLESAPHLRLTQOTTHVEKY 180	
DB	121 WIGYVVENDETSRVARGRREVYVWVRGTCRDYEWYDVLAGQLESAPHLRLTQOTTHVEKY 180	
QY	181 ENEEKKSIHKSSWYDCFNINILIGASAKDKGKSSDDDDDDPPVMOGMMTIYSEDPKSPF 240	
DB	181 ENEEKKSIHKSSWYDCFNINILIGASAKDKGKSSDDDDDDPPVMOGMMTIYSEDPKSPF 240	
QY	241 TKLSARTLOQLKOLMTYKDETLSTPAGHSLSGATLSVSAFDPVLEMLTEIPPTAVY 300	
DB	241 TKLSARTLOQLKOLMTYKDETLSTPAGHSLSGATLSVSAFDPVLEMLTEIPPTAVY 300	
QY	301 FGCPRVGNKKFQQLPDSYPNLNLVLRVNYIDILPIYPVKLMGVNIGIELSDRSKSTFL 360	
DB	301 FGCPRVGNKKFQQLPDSYPNLNLVLRVNYIDILPIYPVKLMGVNIGIELSDRSKSTFL 360	
QY	361 KDSKRPSPDMHNLQALILHVVSQMGVYKGEKRVNKSVALVNSCSPLKKECLVPPAMWVY 420	
DB	361 KDSKRPSPDMHNLQALILHVVSQMGVYKGEKRVNKSVALVNSCSPLKKECLVPPAMWVY 420	

Cy	421	QNKGMVLTNKDGEWTLAPPEDDPTPEPD	447
Db	421	QNKGMVLTNKDGEWTLAPPEDDPTPEPD	447
RESULT 4			
ID	AAG29751	standard; protein: 412 AA.	
XX			
AC	AAG29751;		
XX			
DT	17-OCT-2000	(first entry)	
XX			
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 35451.		
XX			
KW	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	EP1033405-A2.		
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PD	06-SEP-2000.		
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PF	25-FEB-2000;	2000EP-00301439.	
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Query Match 55.0%; Score 1311.5; DB 3; Length 412;
Best Local Similarity 56.0%; Pred. No. 1.7e-124; Indels 27; Gaps 4;
Matches 242; Conservative 72; Mismatches 91;

QY 16 TWPEILGSNANAGLILNPLNDELRLRLRLRCGDFCQVTVDTFINDONSYYGSSRYGKADLL 75
DB 7 SMEELISGKMWDTLPLDPSLRLRLRLRCGDFCQATYDAFVNDGSKYCGASRYGKSSFF 66
QY 76 HKTAFPGGADRFDDVAYIYATKAVSVBPALFKRSRKREKMDRESNWIQYVVVSNDEISRV 135
DB 67 DKVMELENSD-YEVVNFLYATARVSLPEGLILQSOSRSDSMDESNWFGYIAVTSDESKA 125

CC acid (c24:0), linoleic acid (c18:2 (c9, c12)), lutein, lycopene, malate,
CC mannose, methionine, methylgalactofuranoside, methylgalactopyranoside,
CC methylgalactopyranoside, palmitic acid (c16:0), phenylalanine, phosphate,
CC proline, putrescine, pyruvate, raffinose, ribonic acid, shikimate,
CC sinapic acid, stearic acid (c18:0), succinate, sucrose, threonine,
CC triacontanoic acid, tryptophane, tyrosine, ubiquinone, udp-glucose,
CC valine, and zeaxanthine. The plant is selected from maize, wheat, rye,
CC oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola,
CC manihot, pepper, sunflower, flax, borage, safflower, linseed, primrose,
CC rapeseed, turnip rape, tagetes, solanaceous plants, potato, tobacco,
CC eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix*
CC species, oil palm, coconut, perennial grasses, forage crops and Arabidopsis
CC thaliana. The environmental stress is selected from salinity, drought,
CC temperature, metal, chemical, pathogenic and oxidative stresses, or their
CC combinations. The inactivation or down-regulation of the gene is achieved
CC by double-stranded RNA interference (dsRNAi), introduction of an
CC antisense nucleic acid, a ribozyme, an antisense nucleic acid combined
CC with a ribozyme, a nucleic acid encoding a co-suppressor, a nucleic acid
CC encoding a dominant negative protein, DNA- or RNA- or protein-binding
CC factors targeting said gene or -RNA or -proteins, RNA degradation
CC inducing viral nucleic acids and expression systems, systems for inducing
CC a homologous recombination of the genes, mutations in the genes or their
CC combinations. This sequence represents a protein involved in drought
CC tolerance, isolated from Arabidopsis thaliana.

SQ Sequence 412 AA;

Query Match	55.0%;	Score 1311.5;	DB 8;	Length 412;
Best Local Similarity	56.0%;	Pred. NO. 1.7e-124;		
Matches 242;	Conservative 72;	Mismatches 91;	Indels 27;	Gaps 4;

[illegible]

RESULT 8
AAG29750
ID AAG29750 standard; protein; 418 AA

AC	AAG29750;
XX	
DT	17-Oct-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 35450

XX	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
KW	
KM	
KX	
OS	Arabidopsis thaliana.
XX	EP1033405-A2.
PM	
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-00301439.
XX	
PR	25-FEB-1999; 99US-0121825P.
PR	05-MAR-1999; 99US-0123180P.
PR	09-MAR-1999; 99US-0123548P.
PR	23-MAR-1999; 99US-0125788P.
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PR	01-APR-1999; 99US-0127452P.
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PR 25-OCT-1999; 99US-0161404P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 55.0%; Score 1311.5; DB 3; Length 418;
Beet Local Similarity 56.0%; Pred. No. 1.8e-124;
Matches 242; Conservative 72; Mismatches 91; Indels 27; Gaps 4;

QY 16 TWPELIGSNAMAGLNPINDELRELLACGDFCOVTVTFINDNSSYCGSSRGKALL 75
DB 13 SWEELGSKMWDITLIDPDQSLREILILCGDFCOATYAFVNDQSKYCGASRYKSSPF 72
QY 76 HKTAPPGADRFDDVAVYYATKAVSVPEAFILKRSREKMDRESNIGVYVNSDTSRV 135
DB 73 DKWLENSD-YEVVNFYIATARVSLPBGILLQGSRSWRESNWPFIYAVTSDERKXA 131
QY 136 AGRRVYVVMRGCTGDEYEMVDVLGAQLSAPHLRLTQOTTVEKYNEEKSIHKSMPYD 195
DB 132 LGREIYIALRGTSNRYEMVNVLAGRPYSADPLHGP-----EODSGGVGEGTFD 183
QY 196 CPNINLGLASAKDKGSGDDDDDDPKYMOGMMITYSDDPKSPRTKLSARTOLOTUKO 255
DB 184 -----SDSDEBEGCYMLGLMWTITTYISNHPESKFTKLSLSQLAKKXE 226
QY 256 LMTKYDETLSTTFAGHSIGATLSVSAFDIVEN-LTTEIPYTAVFSGCPKVGKKFPOOL 314
DB 227 LILKTKDKKPSIVLTGHSIGATEAVLAVYDIAENSSDVTYALVFCCPGVGNKEPFDE 286
QY 315 FDSYPNINLVLHVRNVYDILPYPVKLMGYVNIIGLELIDSRKSTFLKDSKNPSDMHNLOA 374

Db 287 VMSHKNKILHVRNTIDLTFRYPCGLLGYVDIGINFIVDTRKSPFLSDSRNPGDMHNLQA 346
Qy 375 ILHVNSGMHGVKGEFKVYKNSRVALVYKSCDFLEECIYPAMVNVQKGMVNLKDDGMV 434
Db 347 MLHVNAAGMNGKGFKLWKRSLVYKSCDFLEECIYPAMVNVQKGMVNLKDDGMV 406
Qy 435 LAPPEEDPTPEF 446
Db 407 LAPVEEPVPEF 418
RESULT 9
AAG29752
ID AAG29752 standard; protein: 343 AA.
AC AAG29752;
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 35452.
DE Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; Genetic mapping; gene expression control; promoter;
KM termination sequence.
XX Arabidopsis thaliana.
XX EPI033405-A2.
PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
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PR 23-MAR-1999; 99US-0125788P.
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PR 22-JUL-1999; 99US-0145087P.
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

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Query Match 45.4%; Score 1082; DB 3; Length 343;
 Best Local Similarity 55.5%; Pred. No. 3.6e-101;
 Matches 202; Conservative 63; Mismatches 73; Indels 26; Gaps 3;

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QY 84 ADRFDVAVLYYATKVSVPFAFLIKSRKREKMDRESNWTGIVVVSNDETSRVAGREVVY 143
Db 5 ASDYEYVNFLLYATPABVSLPEGLLLQSQSDMSDRESNMFYIAYTSDERSKALGRREIYI 64
QY 144 VMGTGCDYEMVDVLGNQLESAPHLRTQOTTHVEKXENEEKS IHKSNVDCENILG 203
Db 65 ALRGTSNRYEMVNVNIGARPTSDPLHGP-----EQSGGAVEGITFD----- 108
QY 204 SASKDKGSGDDDDDDPKYMGQWMTIYTSDEPKSPPTKLSARTOLOTKLMTKYXDE 263
Db 109 -----SDSEBECCKMGLGTLITSNHPSKXTKLSLSQLAKIKELLKTXDE 159
QY 264 TLTSTFAGSLGATLSVSAFDIYEN-LTTEIPTAVPFCGPKYKNGKFOOLPSTYNLN 322
Db 160 KPSIVLTGHSLGATEAVLAAYIAENSGSDVPVTAIVFCGPQGVNKEFRDEVNASHKOLK 219
QY 323 VLVHRYNIDILPLYPVLMGYVNIETLEIDRSKSTLKOSKNSPDHNIQALHVSQW 382
Db 220 ILHVRNTIDILTRYPGGLGVDGINFVIDTKSPFLSDSRNGDWHNIQAMHVVAGW 279
QY 383 HGVGKFEKVVNKSVALVNSCDFLKEECVPPAMVYVQNKGVNLKQGEWVLAPEEDP 442
Db 280 NGKKGFEKLMVKRSIALVNSCEFLKAECLVPSWVWEKOKGLIKNGDEWVLAPEEPP 339
QY 443 TPEF 446
Db 340 VPEF 343

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RESULT 10
 ID AAY97308 standard; protein; 348 AA.
 AAY97308;
 XX 03-JAN-2001 (first entry)
 DE Arabidopsis EST showing 55/5% homology with senescence induced.
 XX Senescence-induced lipase; senescence; lipase; antisense; regulation;
 KM modulation; resistance; stress; crop protection; ethylene.
 OS Arabidopsis thaliana.
 XX MO200049164-A1.
 XX PD 24-AUG-2000.
 PF 14-FEB-2000; 2000WO-US003494.
 XX 16-FEB-1999; 99US-00250280.
 PA (SENE-) SENESCO INC.
 PI Thompson JE, Wang T, Hudak K, Hong Y;
 XX WPI; 2000-549277/50.
 DR N-PSDB; AAA5385.
 XX DNA encoding carnation senescence-induced lipase, useful for regulating
 PT the expression of senescence in plants to delay its onset and improve
 PT plant resistance to environmental stress, thus extending shelf-life or
 PT growth period.
 PS Disclosure; Fig 13; 89pp; English.
 XX Insertion of the senescence-induced lipase coding sequence in an
 CC antisense direction in a plant genome can be used to regulate the
 CC expression of senescence in those plants. Alteration of expression of the
 CC senescence-induced lipase gene in plants results in delayed onset of
 CC senescence and improved resistance to environmental stress, thus
 CC extending the plant shelf-life and/or growth period. The genetically
 CC altered plant is useful for producing a new variety or line of plants


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QY      9 GLSKRGPTMPPELLGSAAMGLNLPUNDELRELLRCGDPCQYVYDFFINDQNSYCGSSR 68
Db      21 GWGNVAKKWKELNGLNMYKGLVDPLDPLDRONTINTGELSQATYTGLENNRRSRVAGSCL 80
QY      69 YKADLLHKHTAFPGGADRPDVAAYLATATKAVSVEAFLLKSRSRKEMDRSNSNIGYVVS 128
Db      81 FNRDRPFLSRVDY-SNPNIYEIKFYAMCTVSLPDGFMYKVSLSKAAMRSQNMWGFVAVA 139
QY      129 NDETSRVAGREVVYVWRCTCRDYENVVDVGLGQLESANHLPLRQOQTHVEKVENBEKXI 168
Db      140 TDEGKELLGRRVVAAAMRTIRKVEWVDLDSLVASEIV----- 180
QY      189 HKSWSYDCFNINLLSASAKDKGSGDDDDDDPPKVMQGMWITYTSEDPKSPFTKLSARTQ 248
Db      181 -----LPQSA-----NPCVAGMLSVYTSADPQSGYMKESARHQ 215
QY      249 LQTKLKQOLMTKYKDETLSTFTAGHSLGATLVSVASAFDIENTLTT--IPYAVVFGCPKV 306
Db      216 VLNEVYRLODLYKPEBTSITIGHSHGALATINADIVSNGYRSCCPVASVFGSPRV 275
QY      307 GNKKFQOLFDSYENLVNVLVRNVIDIPLPYPYKVMGYVNIIGLEISDRSTFLXOSKNP 366
Db      276 GNLDFOKAPDSAADRLRLVRNRSPDVVPKMP--KLISYSDVGTBLMDIGESPYLKAPGNP 333
QY      367 SDWNLQAILHVYSGMHGYGSEFFKVVNKSVALVNKSCDFLKEECCLVPAAWVYVQXKGV 426
Db      334 LTHWMECYMHGAVAGAQSGSGGFELLVDBVALVNHGEDALRNEFAPVPBMVYVQXKGV 393
QY      427 LNKQSEWTLAPPEED 441
Db      394 KGKQGRWHLADHEED 408

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XX	ABB92980	standard; protein; 419 AA.
XX	ABB92980	
AC	ABB92980;	
XX		
DT	31-MAY-2002	(first entry)
XX		
DE	Herbicideally active polypeptide SEQ ID NO 2191.	
XX		
KM	Herbicideal; plant; agriculture; herbicide.	
XX		
OS	Arabidopsis thaliana.	
XX		
PN	WO200210210-A2.	
XX		
PD	07-FEB-2002.	
XX		
PF	28-AUG-2001; 2001WO-EP009892.	
XX		
PR	28-AUG-2001; 2001WO-EP009892.	
XX		
PA	(FARB) BAYER AG.	
PI	Tietjen K, Weidner M;	
XX		
DR	WPI; 2002-269010/31.	
XX		
PT	Identifying plant target proteins for herbicideally active compounds,	
XX	comprising aligning and comparing nucleic acid or amino acid sequences	
PT	from plant with nucleic acid or amino acid sequences from non-plant	
XX	organisms.	
XX		
PS	Claim 5; SEQ ID NO 2191; 261pp + Sequence Listing; English.	
XX		
CC	The invention relates to identifying target proteins (ABB90790-ABB94016)	
XX	for herbicideally active compounds, comprising aligning and comparing	
CC	nucleic acid or amino acid sequences from plant with nucleic acid or	
XX	amino acid sequences from non-plant organisms using suitable search	
CC	parameters, where plant sequences having an E-value greater by a factor	

CC of 3 than the E-value of most similar non-plant sequences are selected
CC The polypeptides or nucleic acids encoding them are useful for
CC identifying modulators. The identified modulators are useful as
CC herbicides

SQ Sequence 419 AA;

Query Match	33.1%;	Score 789.5;	DB 5;	Length 419;
Best Local Similarity	37.8%;	Pred. No. 3.8e-71;		
Matches 168;	Conservative 77;	Mismatches 137;	Indels 63;	Gaps 8;

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0Y 17 WPELLGSNAAGLNLPLNDELRELLRCGDPCQVYDFEINDQNSYCCSSRYGKADLLH 76
Db 23 WRDLSCGHMKMGMLQPLDQDLREYIIHGHMAQGYDTFNINTEQOFAGASYSRDFFA 82
0Y 77 KT---APFGADRPDVAVLYATKAGVPEAFLLKSRSREKWDRESNVIYGVVSNDET 132
Db 83 KVGLEIAR--YTKKVKTKFYATSDIHVPBSFLFPISREQMSKESNMGYAVLVDQOG 140
0Y 133 SRVAGRPVVYVMGTGRDYEMVDVLGAQLSAAHLRLRQCTTHKEKVENEEKSIHKSS 192
Db 141 TALGRROIVSMKGSVOPLEWVEDEFEGLVNA----- 173
0Y 193 WYDCFNINLLGSASKDKGSGDDDDDDDPKVMQGMNTIYTSDDPKSPPTKLSARLOLTK 252
Db 174 -----IKIFG-----BENDQVQHMGVSYISMQDEKSPFTKTNARDQVLNE 215
0Y 253 LKQMLTKYKDETLTITPAGHSLGATLSVVSADFYEN-----LTTEIPTYAVVFGCP 304
Db 216 VGRLEEKXKBEVSIITCGHSLGALATLSADTYANGYRPKSRBDKCPYTAFFFAFP 275
0Y 305 KVGKKKFOOLFDSYPNLNLVHVBNVYIDLPLPYVYLMGVNIGIELEIDSRKSTFLKDSK 364
Db 276 RVGSDRKRKLFSSGLEDINVLRTNRLPDVYIPIYP--IGTSVGDDEFPIDTRKSPYMKSG 333
0Y 365 NPSDMHNLQALILHAVSGMHGV-KGB-FKVNKRKSVALVYKSCDFLKEECLVPPAMVYON 422
Db 334 NLAFFHCLEGIYHGAQGTQTNKADLFLDVERBAIGLVNKSVDGKDECMVPGKRVLKN 393
0Y 423 KGMVLNDGCVNLARPEEDPTPEPD 447
Db 394 KGMQODDGSWELVDHEITDNEDD 418

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	RESULT	15
XX	AA97305	
ID	AA97305	standard; protein; 418 AA.
XX		
AC	AA97305,	
XX		
DT	03-JAN-2001	(first entry)
XX		
DE	Senescence-induced lipase (arlip).	
XX		
KW	Senescence-induced lipase; senescence; lipase; antilipase; regulation	
XX	modulation; resistance; stress; crop protection; ethylene.	
OS	Arabidopsis thaliana.	
XX		
PN	WO200049164-A1.	
PD		
24-AUG-2000.		
PF	14-FEB-2000;	2000MO-US003494.
PR	16-FEB-1999;	99US-00250280.
PA	(SENE-) SENESCO INC.	
PI	Thompson JE, Wang T, Hudak K, Hong Y;	
WP1;	2000-549277/50.	

PT DNA encoding carnation senescence-induced lipase, useful for regulating the expression of senescence in plants to delay its onset and improve PT plant resistance to environmental stresses, thus extending shelf-life or PT growth period.

PS Disclosure; Page 76-78; 89pp; English.

Insertion of the senescence-induced lipase coding sequence in an antisense direction in a plant genome can be used to regulate the expression of senescence in those plants. Alteration of expression of the senescence-induced lipase gene in plants results in delayed onset of senescence and improved resistance to environmental stresses, thus extending the plant shelf-life and/or growth period. The genetically altered plant is useful for producing a new variety or line of plants where the alteration is stably transmitted from generation to generation. This method of regulation is advantageous over prior senescence modulating technologies since prior methods were only applicable to a limited range of plants, e.g. to plants that are ethylene-sensitive. The antisense regulation method is applicable to all types of plants, regardless of ethylene sensitivity.

SQ Sequence 418 AA;

Query Match	32.5%;	Score	775;	DB 3;	Length	418;	
Best Local Similarity	37.5%;	Pred. No.	1.2e-69;				
Matches 167; Conservative	76;	Mismatches	138;	Indels	64;	Gaps	9;

Qy	17	PELLGSNMAQALLNPINDELRELLRCGDFCQVUTDFINDONSVCSSRGKADLH	76
Db	23	WDLTSGONNMKMLQDLPDLDBREYLIHHGEMAOAGYDFININIESQFAGASISYRKDFFA	82
Qy	77	KT----APFGADREDVVAVLYATAKVSYPEAFELKRSREKMDRESNMIGYVVSNDT	132
Db	83	KVGLFIAPH--YTKVKATKFIATSDIHVSEFLLPISREGSKESNMWGYAVLTDQG	140
Qy	133	SVAGRREYVVVWRCGCRDEYEWVDVGAQLESHPLLRQOQTHHVEKVENBEKKS1HKSS	192
Db	141	TALLERRDVLVWMSGVQPLEWEDEFGLVNA-----	173
Qy	193	WYDCENINILSGASKDKGSGDDDDDDPKVMGMNTIYTSBDPKSPFTYLSARTOLOTK	252
Db	174	-----IKIFG-----ERNDOYQHOGWISYMSQDERSFFTTNARDQYLRE	215
Qy	253	LKQMTKYKDEFLSTFAGHSICATLSVVSAPDIVEN-----LTTLEPVAUVFGCP	304
Db	216	VGRLEEKYKDEEVSITICHSIGALATSDAIDIVANGVNRPKSRDPKSCPVIAPFAPSP	275
Qy	305	KVGNKKFQOLFDSYPLNVLVHNVNVDLPPLYEVKLMGYNIGIELEIDRSKSTFLDOSK	364
Db	276	RKGGSDFRKLDFEGLEDIRVLRNTLNDVLFPIYR--IGYSEVDEDFIDTRKSPYMKSPG	333
Qy	365	NPSDWHNLQALLHHVVSQMGHV--KGE-FKVYNKRSVALVNKSCDFLKECLVPPAMVVON	422
Db	334	NLATFHLCLEGYLHVAGTOGTNKADFLRLDVERALIGLVNKSVDGLKDECVVPGKMRVLKN	393
Qy	423	KGMVTLNKQSENVLLAPREDDPTPEFD	447
Db	394	KG-AAQDDGSGWELVHDHIDNEJLD	417